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APPLICANT: Russell, David W.
APPLICANT: Tian, Hui
TITLE OF INVENTION: Endothelial PAS Domain Protein
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 BUSH STREET, SUITE 3200
CITY: SAN FRANCISCO
STATE: CALLFORNIA
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CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 17-JAN-1997
CLASSIFCATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN: RICHARD A
REGISTRATION NUMBER: 35,627
REFERENCE/DOCKET NUMBER: UTSD:1229
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 7:
                         US-08-785-241-5
US-09-374-454-4
US-09-374-454-6
US-09-374-454-6
US-09-374-454-6
US-08-480-4738-3
US-09-235-217-3
US-09-235-217-3
US-09-235-217-4
US-09-155-310A-5
US-09-155-310A-5
US-09-155-310A-5
US-09-156-460B-17
US-09-156-460B-17
US-09-156-460B-18
US-09-156-460B-18
US-09-374-454-31
US-09-374-454-31
US-09-374-454-31
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US-09-374-454-21
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US-09-150-460B-15
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 7, Application US/08785241 Patent No. 5695963 GENERAL INFORMATION:
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LENGTH: 810 amino acids
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MEDIUM TYPE:
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-Q-Cq012_1/102FO2_59001/050996591/runat_02122002_152659_5635/app_query.fasta_1.1287
-Q-Cq012_1/102FO2_59001/050996591/runat_02122002_152659_5635/app_query.fasta_1.1287
-Q-Cq012_1/102FO2_59001/05099696591_Fasta_1 -SIND*-1.102FIX*-ai -MINMATCH-0.1 -LOOPCL-0.
-LOOPEXT=0 -UNITS-bits -START=1 -END*-1 -MATRIX*-blosum62 -TRAMS-human40.cdi
-LIST*-45 -DOCALIGN*-200 -THR_SCORE=-pet -THR_MAX*-100 -THR_MIN-0 -ALIGN*-126
-UOSE*-UOSE*-LOOTEM*-pto -NORM*-ext -HEAPSIZE*-500 -MINIEN*-0 -MAXLEN*-200000000
-USER-US09996791_ECGN_11_9_Erunat_0212002_152659_5635 -NCPU*-6 -ICPU*-3
-NOA_XLDXY -NO_MANP -LARGEODERY -NGC_SCORES*-0 -WAIT -LONGLOG -DEV_TIMEOUT*-120
-WARN_TIMEOUT*-30 -THREADS*-1 -XGAPOP*-10 -XGAPEXT*-0.5 -FGAPOP*-6 -FGAPEXT*-7
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/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                   OM nucleic - protein search, using frame_plus_n2p model
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US-09-438-833-4
US-09-438-833-5
US-09-438-833-12
US-08-785-241-6
US-08-915-213-2
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US-09-148-547-2
US-09-235-217-2
US-09-380-662-23
US-09-438-833-1
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Maximum Match 100%
Listing first 45 summaries
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Xgapop 10.0 , Ygapext (
Ygapop 10.0 , Ygapext (
Fgapop 6.0 , Fgapext Delop 6.0 , Pgapext
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Maximum DB seq length: 2000000000
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                                                                     Length:
Matches:
Conservative:
Mismatches:
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Gaps:
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TITLE OF INVENTION: Protein variants
FILE REFERENCE: 1848
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                                                                     9.71e-52
607.50
67.65%
53.78%
30.22%
        single
                TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-785-241-7
STRANDEDNESS: Sin
                                                                                         Percent Similarity:
Best Local Similarity:
                                                            Alignment Scores:
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                                                                                                                Query Match:
                                                                      Pred. No.:
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195 ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
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Mismatches:
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                                                                                                      OTHER INFORMATION: Description of Artificial & OTHER INFORMATION: 1-245 of human HIF-1 alpha
                                                                                                                                                                     Length:
Matches:
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CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VEr. 2.1
SEQ ID NO 3
LENGTH: 245
                                                                             ORGANISM: Artificial Sequence
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606.50
68.07%
54.20%
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Best Local Similarity:
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DB:
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ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr 212
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Matches:
Conservative:
Mismatches:
Indels:
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GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn
TITLE OF INVENTION: Protein variants
FILE REFERENCE: 1848
CURRENT APPLICATION NUMBER: US/09/438,833
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 4
LENGTH: 330
                                                                                                                                                    ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                               8.51e-52
606.50
68.07%
54.20%
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Best Local Similarity:
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213 LysLysProProMetThrCysLeuValLeuIleCysGluProIlePro
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Mismatches:
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TITLE OF INVENTION: Protein variants
FILE REFERENCE: 1848
CURRENT APPLICATION NUMBER: US/09/438,833
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
                                                                                       Sequence 5, Application US/09438833 Patent No. 6436654 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
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OTHER INFORMATION:
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US-09-438-833-5
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Best Local Similarity:
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                                                                    213 LysLysProProMetThrCysLeuValLeuIleCysGluProIlePro 228
                                                      TCCGAGCCTCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCC 741
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Matches:
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Fatent No. 643654
Reneral INFORMATION:
TITLE OF INVENTION: Protein variants
FILE REFERENCE: 1848
CURRENT APPLICATION NUMBER: US/09/438,833
CURRENT APPLICATION NUMBER: US/09/438,833
SOFURMER OF SEQ ID NOS: 15
SOFURMER PATENTING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 15
SOFURMER: PATENTIN VET. 2.1
SSO ID NO 12
LENGTH: 813
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195 ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
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APPLICANT: Russell, David W.
APPLICANT: Tian, Hui
TITLE OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version #1.30
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/785,241
FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
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NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4342
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/08785241
Patent No. 5695963
GENERAL INFORMATION:
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INFORMATION FOR
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195 ThrGlyHisTleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
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                                                                       GCAGCAGGTGGAAAAAGGGGGAGAG----------CCACTGGACGCCTGCTACCT
34 SerGluValPheTyrGluLeuAlaHisGlnLeuProLeuProHisAsnValSerSerHis
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TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF WUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Patentin Release #1.0, Version #1.30
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rAspAsnValAsnLysTyrMetGlyLeuThrGln-----
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ATTORNEY/AGENT INFORMATION:
NAME: Halle, Lisa A.
REGISTRATION NUMBER: 38,347
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
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FILING DATE: 06-JUN-1995
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OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION:
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HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
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Matches:
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Patent No. 6020462
GENERAL INFORMATION:
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606.50
68.07%
54.20%
30.17%
                                    826 amino acids
FORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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                                                     amino acid
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Best Local Similarity:
                                                                                     MOLECULE TYPE:
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                                                                      TOPOLOGY:
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GGAAAATGTCAGCAAGCACCTGGGCCTCAGTCGACCTCTGTTCCTCCTCCTGATA 393
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rAspAsnValAsnLysTyrMetGlyLeuThrGln--------124
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1129
333
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                                                                                                                                                    SOFTWARE: Patentin release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,213 FILING DATE: 20-AUG-1997 CLASSIFICATION: 514 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/480,473 FILING DATE: 06-JUN-1995 ATTORNEY/AGENT INFORMATION:
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Indels:
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length:
Matches:
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                                                                                                    COMPUTER READABLE FORM:
BDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                      NAME: Halle, Lisa A.
REGIZTRATION NUMBER: 38,347
REPRENCE/DOCKET NUMBER: 0726;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5079
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
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454 ITTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGGCCGAACCTG
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195 ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
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                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09148547

Patent No. 6124131

GENERAL INFORMATION:
APPLICANIT: Semenza.
TITLE OF INVENTION: Hypoxia Inducible Factor-1 and Methods of Use
FILE REFERENCE: 07265/151001
CURRENT APPLICATION NUMBER: US/09/148,547

UNMBER OF SEQ ID NOS: 2
SCHWARE PATENT PATENT OF SEQ ID NOS: 2
SEQ ID NO 2
LENGTH: 826
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Mismatches:
Indels:
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606.50
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Best Local Similarity:
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Pred. No.:
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US-09-896-791B-2 (1-1100) x US-09-235-217-2 (1-826)
------Phe--GluLeuThrGlyHisSerValPheAsp 134
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                                               454 ITTAICCAICCCIGIGACCAAGAGGAACTICAAGACGCCCIGACCCCCAGGCCGAACCIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Semenza, Gregg L.
TITLE OF INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF USE
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                  213 LysLysProProMetThrCysLeuValLeuIleCysGluProIlePro 228
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SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Mismatches:
Indels:
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Matches:
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APPLICATION NUMBER: US 08/480,473
FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/235,217 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 0726:
TELECOMMUNICATION INFORMATION:
TELEFAN: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2, Application US/09235217
Patent No. 6222018
GENERAL INFORMATION:
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STATE: CA
COUNTRY: USA
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Best Local Similarity:
Query Match:
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APPLICANT: Caniggia, Isabella
APPLICANT: Caniggia, Isabella
APPLICANT: Caniggia, Martin
APPLICANT: Lye, Seephen
TTYLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF TROPHOBLAST
FILE REFERENCE: 11757.38USWO
CURRENT APPLICATION NUMBER: US/09/380,662
CURRENT APPLICATION NUMBER: DCT/CA98/00180
PRIOR FILING DATE: 1998-03-05
PRIOR FILING DATE: 1998-03-05
NUMBER OF SEQ ID NOS: 24
NUMBER OF SEQ ID NOS: 24
NUMBER: Patentin version 3.0
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195 ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
               14 SerSerGluArgArgLysGluLysSerArgAspAlaAlaArgSerArgArgSerLysGlu
                                                                          229 GCAGCAGGTGGAAAAAGGGGGGAGAG-------CCACTGGACGCCTGCTACCT
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LENGTH: 826
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| ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
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         Length:
Matches:
Conservative:
Mismatches:
                                                                                   US-09-896-791B-2 (1-1100) x US-09-380-662-23 (1-826)
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GENERAL INFORMATION:
APPLICANT: Pharmacia & Upjohn
TITLE OF INVENTION: Protein variants
FILE REFERENCE: 1848
CURRENT APPLICATION NUMBER: US/09/438,833
CURRENT FILING DATE: 1999-11-12
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
                                                     Indels:
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Patent No. 6436654
        1.23e-51
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                            Percent Similarity:
Best Local Similarity:
Alignment Scores:
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LENGTH: 826
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US-09-438-833-1
                                                   Query Match:
          Pred. No.:
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GENERAL INFORMATION:
APPLICANT: The Johns Hopkins University School of Medicine
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Mismatches:
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DATABASE ENTRY DATE: 1995-06-28
                         Sci. U.S.A.
                                                                                                                                 1.23e-51
606.50
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54.20%
                          Proc. Natl. Acad.
            PUBLICATION INFORMATION
                                                                                                                                                           Percent Similarity:
Best Local Similarity:
                                                  5510-5514
Homo
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                                                                                            US-09-438-833-1
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VOLUME: 92
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135 PheThrHisProCysAspHisGluGluMetArgGluMetLeuThrHisArgAsnGlyLeu 154
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                                                                                                                                                                                                                                                               Sequence 5, Application US/08785241
Patent No. 5695963
GENERAL INFORMATION:
APPLICANT: MCKnight, Steven L.
APPLICANT: Tian, Hul
ITLE OF INFORMATION:
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: SCIENCF . --
STREFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Mismatches:
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FILING DATE: 17-JAN-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 4-2.
ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UTSD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
TELEPHONE: (415) 343-4342
INFORMATION FOR SED ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 875 amino acids
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65.25%
51.35%
29.00%
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TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: SAN FRANCISCO STATE: CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
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Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USA
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                                                                                                                                                                                                                                                                                                     US-08-785-241-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 CTGGACAAGGCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGC 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             274 GAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATGGCTTACCTGTC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGAAAATGTCAGCAAGCACCTGGGCCTCAGTGGACCTCTGTTCCTCCTCCTCGATA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATAACCCCCACTCCTGGTACCAATTTCTCTGGAGCTCATTGGACACAGTATCTTTGAT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGGCCGAACCTG 513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                USE
   INVENTION: HYPOXIA INDUCIBLE FACTOR-1 AND METHOD OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           826
129
33
48
28
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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Mismatches:
Indels:
Gaps:
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                                               E: Fish & Richardson P.C. 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                    APPLICATION NUMBER: PCT/US96/10251
FILING DATE: 06-JUN-1996
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38, 347
REFERENCE/DOCKET NUMBER: 07265/053W01
TELECHONE: 619/678-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
Matches:
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68.07%
54.20%
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                             COMPUTER READABLE FORM:
                               CORRESPONDENCE ADDRESS:
 TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                               La Jolla
                                                                                                                USA
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                                               ADDRESSEE:
STREET: 42
CITY: La J
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                                                                                             STATE: CA
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                                                                                                                                                                                                                                                       GAACTICAAGACGCCCTGACCCCCAGG-----CCGAACCTGTCAAAGAAGAAGCTGGAA 531
                                                                                                                                                                                                                                                                                                               591
                                                                                                                                                                                                                                                                                                                                                        162 ValSerThrGluArgAspPhePheMetArgMetLysCysThrValThrAsnArgGlyArg 181
GACGCGCCCCCAGCCGCCAGCCAGACGGAGGTGCTGTACCAGCTGGCGCACACT 138
                                                                                                                                                                                                                                                                                                                                                                                      202 ValTyrAsnAsnCysProProHisSerSerLeuCysGlySer-----LysGluProLeu
           CTGCCCTTTGCGCGCGCGTCAGCGCGCACCTGGACAAGGCCTCCATCATGCGCCTCACA
                                                    199 ATCACCTACCTGCGCATGCACCGCCTC-----TGCGCAGCAGGTGGAAAAAGG
                                                                                               47 GGGAGAG------CCACTGGACGCCTGCTACCTGAAGGCCCTGGAGGGTTTCGTCAT
                                                                                                                                                                       532 GCCCCAACAGAGCGCCACTTTTCCCTGCGAATGAAGAGCACGCTCACCAGCAGAGGGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Lee, Mu.En
APPLICANT: Macmura, Koji
APPLICANT: Macmura, Koji
APPLICANT: Macmura, Koji
TITLE OF INVENTION: METHODS OF MODULATING OF ANGIOGENESIS
FILE REPRENCE: 05433/037001
CURRENT PLLING DATE: 1999-08-13
FEARLIER APPLICATION NUMBER: US 60/096,515
EARLIER APPLICATION NUMBER: US 60/096,515
FARLIER PELING DATE: 1999-08-14
NUMBER OF SEQ ID NOS: 22
SOFTWARE: FRASESQ for Windows Version 4.0
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
Pred. No.:
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LENGTH: 485
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| IleSerPheLeuArgThrHisLysLeuLeuSerSerValCysSer-GluAsnGluSerGl
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37
58
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           Conservative:
                      Mismatches:
Indels:
                                                                  US-09-896-791B-2 (1-1100) x US-09-374-454-4 (1-485)
 Matches:
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Query Match:
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Scoring table:

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Sequence 4, Appliance sequence 13, Appliance 659, Appliance 659, Appliance 6113, Appliance 6113, Appliance 6113, Appliance 613, Appliance 126, Appliance 126, Appliance 604, Appliance 604
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Sequence 2, Appli
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0.05-09-764-868-504

0.05-09-764-868-604

0.05-09-764-853-604

0.05-09-764-853-604

0.05-09-764-853-793

2.05-10-001-843-143

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0.05-09-864-1561

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0 US-09-833-790-235
2 US-10-028-158-23
0 US-09-923-684-4
0 US-09-923-684-3
0 US-09-925-297-863
0 US-09-925-302-659
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Matches:
Conservative:
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US-09-764-846-251
US-09-925-300-1453
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US-09-764-846-186
US-09-764-846-187
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Patent No. US20020165140A1
GERERAL INFORMATION:
GERERAL INFORMATION:
APPLICANT: Bertilsson, Gran
APPLICANT: Bertilsson, Gran
APPLICANT: Poellinger, Lorenz
TITLE OF INVENTION: SCREENING METHODS
FILE REFERENCE: 13425-040001
CURRENT APPLICATION NUMBER: US/09/896,791B
CURRENT APPLICATION NUMBER: 60/217,570
PRIOR APPLICATION NUMBER: SE 0002551-0
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-07-06
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.93e-120
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         ; ORGANISM: Mus musculus
US-09-896-791B-3
      \begin{array}{c} \mathbf{c} \\ \mathbf{
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LENGTH: 307
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-MODEL=frame+.n2p.model.-DEF-x1p
-OG-/Cgn2_1/USPTO_spool/US0996791/runat_02122002_152700_5721/app_query.fasta_1.1287
-OG-/Cgn2_1/USPTO_spool/US09996791/runat_02122002_152700_5721/app_query.fasta_1.1287
-OG-/Cgn2_1/USPTO_spool/US09996791/runat_021200_1 - MATRIX=Dlosum62
-LOOPCLL0 -LOOPEXT=0 -UNITS=blts -START=1 -END=-1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCAL-LGOAL -OUFR=CORE-pct - THR_MAX=10
-THR_MIN-0 -ALIGN=15 -MODE-LOCAL -OUFR=TW-pto -NORM=ext -HEAPSTZE=500 -MINLEN-0
-MAXLEN-200000000 -USR=US09996791_GCGN_1].5 @runat_021202_152700_5721
-NCPU=6 -ICPU=3 -NO_XLPXY -NO_MMAP -LANGEQUERY -NGC_SCORES=0 -WAIT -LONGLOG
-DEV_INMEOUT=120 -WARN_TIMEOUT=0 -THREADS=1 -XGAPOP=10 -XGAPOR=10 - XGAPOP=6
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                               GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                                                                                                                        OM nucleic - protein search, using frame_plus_n2p model
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Mismatches:
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         APPLICANT: Bangur, Chaitanya S.
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Lodes, Michael A.
APPLICANT: Fanger, Gary
APPLICANT: Todes, Michael A.
APPLICANT: Carter, Darrick
APPLICANT: Retter, Darrick
APPLICANT: Retter, Marc
APPLICANT: Fan, Liqun
APPLICANT: Fan, Liqun
APPLICANT: Mang, Aljun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
CURRENT APPLICATION NUMBER: US/09/736,457
CURRENT FILING DAFE: 2000-12-13
NUMBER OF SEQ ID NOS: 1864
SOFTWARE: FastSEQ for Windows Version 3.0
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                                                                                                                                                 Sequence 330, Application US/09902941

Patent No. US20020172952A1

GENERAL INFORMATION:
APPLICANT: Henderson, Robert A.
APPLICANT: Handerson, Jeffrey C.
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Johnson, Jeffrey C.
APPLICANT: Retter, Marc W.
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Carter, Darrick
APPLICANT: Eanger, Cary R.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Bangur, Chaltanya S.
APPLICANT: Markinon: ComPositions AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG
TITLE OF SEQ ID NOSE: 2001-07-10
NUMBER OF SEQ ID NOS: 2002
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 330
LENGTH: BAP
                                                                         694 TCCGAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCC 741
                                                                                       213 LysLysProProMetThrCysLeuValLeuIleCysGluProIlePro 228
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Mismatches:
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Best Local Similarity:
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APPLICANT: POELLINGER, LOTENZ
APPLICANT: POELLINGER, LOTENZ
APPLICANT: POELLINGER, Teresa
APPLICANT: POELLINGER, Teresa
APPLICANT: PORTICANT: DOSG
TITLE OF INVENTION: MECHANISM OF CONDITIONAL REGULATION OF THE HYPOXIA-INDUCIBLE F
TITLE OF INVENTION: THE VON HIPPEL-LINDAU TUMOR SUPPRESSOR PROTEIN
FILE REFERENCE: 3143/4900
CURRENT APPLICATION NUMBER: US 60/922,958
CURRENT FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 60/223,480
PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN VETSION 3.0
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                                    -----Phe--GluLeuThrGlyHisSerValPheAsp 134
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195 ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
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394 CATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGACACAGTATCTTTGAT
                                                                               454 TTTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGGCCGAACCTG
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Mismatches:
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; Patent No. US20020048794A1
; GENERAL INFORMATION:
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US-09-922-958-4
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Best Local Similarity:
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LENGTH: 826
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Fatent No. US20020066288a1
Fatent No. US20020066288a1
FAPELICANT: Lodge, Michael J.
APPLICANT: Secrist, Heather
APPLICANT: Secrist, Heather
APPLICANT: Fan, Liqun
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: COMPOSITIONS AND JAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.512
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT APPLICATION NUMBER: US/09/833,790
CURRENT APPLICATION NUMBER: US/01-04-11
NUMBER OF SEQ ID NOS: 440
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches:
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LENGTH: 826
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Patent No. US20020110833A1
GENERAL INFORMATION:
APPLICANT: Caniggia, Isabella
APPLICANT: Caniggia, Isabella
APPLICANT: Lye, Stephen
TITLE OF INVENTION: METHODS TO DIAGNOSE A REQUIRED REGULATION OF
TITLE OF INVENTION: TROPHOBLAST
FILE REPRENCE 11757.3808W0
CURRENT APPLICATION NUMBER: US/10/028,158
CURRENT FILING DATE: 1999-12-21
PRIOR APPLICATION NUMBER: PCT/CA98/00180
PRIOR FILING DATE: 1999-12-21
PRIOR PILING DATE: 1998-03-05
PRIOR FILING DATE: US 60/039,919
               74 AspAlaGly-AspLeuAspIleGluAspAspMetLysAlaGlnMetAsnCysPheTyrLe
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Matches:
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Mismatches:
                                                                  GCAGCAGGTGGAAAAAGGGGGGAGAG----
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SOFTWARE: PatentIn version 3.0
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US-10-028-158-23
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Best Local Similarity:
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LENGTH: 826
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	pAspMetLysAla		අ	42 IleIleA
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	SGAAAATGTCAGCAAGCACCTGGGCCTCAGTCAGTGGACCTCTGTTCC	CTCCTCCCTGATA 393	δδ 7	
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	CATAACCCCACTCCTGGTACCAATTCTCTCTGGAGGTCATTGGACACAGTATCTTTGAT	CAGTATCTTTGAT 453	λ qα	322 GGCTTAC : 101 eMetTyr
	PheGluLeuThrGlyHie	sSerValPheAsp 134	λO	
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	LeuThrSerArgGlyArgThrMetAsnIleLysSerAlaThrTrpLysValLeuHisCys	sValleuHisCys 194	<u>a</u>	
Ē · · · B	TCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCTGCCGGGAGCCCTCGC	AGCCCTCGC	oy G	559 CGAATGAA 163 ArgMetLy
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9	1,0001 / 10001		qa	201 TyrAspS
0 +	4, Application 05/05525064 . US2000081613A1		Qy	709 CAATGCC
4 Z G	CALL		qa	220
4 124	G .		Qy	763
- (CURRENT AFFLICATION NUMBER: US/US/9/923,084 MINTERNT FILING DATE: 2001-09-17 MINTER OF SEC 12 MAG: 15		q	233 MetPheA
) III (r SEQ ID NOS: 10		Qy	778
LENGTH:	TD NO 4 FIGTH: 570 VDF: DDT		q _O	253 ThrGlyT
, CO C	1115. TAT TOTALSMISM: Homo sapiens 00-073-684-4		οy	802 ACCTTAT
o o			qa	273 AspvalP
Pred. No.:	7.33e-17 Length: 570		Qy	859

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|rgAlaSerLeuAspLeuLiysLeuIlePheLeuAspSerArgValThrGluVal 252
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              Conservative:
Mismatches:
Indels:
Gaps:
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                             ATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGCGCAGCAGGT-----
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Factor No. US20020081613A1

GENERAL INFORMATION:

APPLICANT: Narayanan, Ramaswamy

TITLE OF INVENTION: ASSOCIATION OF SIM2 WITH CANCER

FILE REFERENCE: 6818-24

CURRENT APPLICATION NUMBER: US/09/923,684

CURRENT FILING DATE: 2001-09-17

NUMBER OF SEQ ID NOS: 16

SOFTWARE: Patentin version 3.1

SEQ ID NO 3
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Conservative:
Mismatches:
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311.00
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ORGANISM: Homo sapiens
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Best Local Similarity:
Query Match:
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                                         AGTATCTTTGATTTTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCC
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Patent No. US20020081659A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION:

CURRENT APPLICATION NUCLEIC Acids, Proteins and Antibodies

FILE REFERENCE: PA105

CURRENT APPLICATION NUMBER: US/09/925,297

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05989

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 928
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OTHER INFORMATION:
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                                            PREMINES.

ORGANISM: Homo sapiens

PREMIURE:

NAME/KEY: SITE

LOCATION: (77)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (80)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

NAME/KEY: SITE

LOCATION: (88)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COCATION: (81)

COCATION: (91)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COCATION: (91)

COTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids

COCATION: (91)
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Squence 559 Application US/09925302

Fatent No. US20020044941A1

SENERAL INFORMATION:

APPLICANT: ROSEN et al.

ITILE OF INVENTION: Nucleic Acids, Proteins and Antibodies

CURRENT APPLICATION NUMBER: US/09/925,302

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/US00/05918

PRIOR PILING DATE: 2000-03-08

PRIOR PILING DATE: 1999-03-12

NUMBER OF SEO ID NOS: 896

SOFTWARE: Patentin Ver. 2.0

SEO ID NO 659
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Matches:
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Mismatches:
Indels:
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61.46%
48.96%
11.07%
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 863
LENGTH: 99
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (186)
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE
LOCATION: (376)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Xaa equals any of the naturally occurring L-amino acids
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                                                                                                                                                                                                                                                                                                                            Sequence 1139, Application US/09764864

Fatent No. US20020132753A1

GENERAL INFORMATION:

APPLICANT: Rosen et al.

TITLE OF INVENTION: NUMBER: US/09/764,864

CURRENT APPLICATION NUMBER: US/09/764,864

CURRENT FILING DATE: 2001-01-17

Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1139
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                ) NAME/KEY: SITE
; LOCATION: (260)
; OTHER INFORMATION:
US-09-925-302-659
                                                                                                                                                                  Percent Similarity:
Best Local Similarity:
Query Match:
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LOCATION: (485)
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LOCATION: (491)
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LOCATION: (465)
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                                                                                                                  Alignment Scores:
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191 ValAlaLysValLysGluGlnLeuSerSerPheAspIleSerProArgGluLysLeulle 210
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251 GluHisGlyCysLeuProAsnSerLysLysLysGluHisArgLysPheTyrThrIleHis 270
                                                                                                                                                                                             97 CGCAGCCAGGAGCGGAGGTGCTGTACCAGCTGGCGCACACTCTGCCCTTTGCGCGCGGGC 156
                                                                                                                                                                                                                                                                                                                                                            114 ------SerLeuLysGlyLeuThrAsnSerTyrValGlySerAsnTyrArgPro 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         472 CAAGAGGAACTTCAAGACGCCCTG----513
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 TGCTCAGGACATATGAGGGCCTACAAGCCC-----CCTGCACAGACTTCCCCTGCCGGG 684
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                                                                                         35 GlyThrArgProThrAlaMetGlySerPheSerSerHisMetThrGluPheProArgLys 54
                                                                                                                                96
                                                                                                                                                             55 ArglysGlySerAspSerAspProSerGlnGluAlaHisSerGlnThrGluLysArgArg 74
                                                                                                                                                                                                                          75 ArgAspLysMetAsnAsnLeulleGluGluLeuSerAlaMetIleProGlnCysAsnPro 94
                                                                -CTGCAG 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          157 GTCAGCGCGCACCTGGACAAGGCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATG
                                                                                                                                                                                                                                                                                                                             217 CACCGCCTCTGCGCAGCAGGTGGAAAAAGGGGGGAGAGCCACTGGA---------
                                                                                                                                                                                                                                                                                                                                                                                            532 GCCCCAACAGAGCGCCACTTTTCCCTGCGAATGAAGAGCACGCTCACCAGC
                                                                                                                             37 CGCGTGAGGTCGAACACCGAGCTGCGGAAGGAGAAGTCGCGGGACGCGGCCCGCAGCCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    745 CTC---CCCTTCCACGATGGTGCTACTCTGGGTCTTCCACAGGAG 786
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11
                              US-09-896-791B-2 (1-1100) x US-09-764-864-1139 (1-591)
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Patent No. US20020048763A1
GENERAL INFORMATION:
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                                                              GGCACGAGGCCCATGGCGTTGGGG---
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TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
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N: EXPRESSED IN LUNG, SIGNAL = 2.9
N: EXPRESSED IN HELA, SIGNAL = 2.7
N: EXPRESSED IN HEARY, SIGNAL = 2.7
N: EXPRESSED IN FETAL LIVER, SIGNAL = 2.8
N: EXPRESSED IN SETAL LIVER, SIGNAL = 3
N: EXPRESSED IN BORIT LIVER, SIGNAL = 2.9
N: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
N: EXPRESSED IN BONE MARROW, SIGNAL = 2.9
N: EXT_HUMAN HIT: AI360153.1, EVALUE 1.00e-21
N: SWISSPROT HIT: Q24119, EVALUE 5.00e-21
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Matches:
Conservative:
Mismatches:
Indels:
                                                                                                                                                FILE REFERENCE: Aeomica X.1
CURRENT APPLICATION NUMBER: U$/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: U$ 60/207,456
PRIOR APPLICATION NUMBER: U$ 60/207,456
PRIOR APPLICATION NUMBER: U$ 09/632,366
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-06-07
PRIOR PRELICATION NUMBER: U$ 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR PLING DATE: 2000-10-04
PRIOR PLING DATE: 2000-09-27
PRIOR PELING DATE: 2000-09-27
PRIOR PELING DATE: 2001-01-30
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Rank, David R.
Hanzel, David K.
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Best Local Similarity:
Query Match:
DB:
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192 CCTCACAATCAGC-
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                                                                                                                                                                                                                                                                                                                                                                                                                            LOCATION: (488)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (490)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (494)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids NAME/KEY: SITE LOCATION: (495)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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                    -- CAGCGCGCACCTGGACAAGGCCTCCATCAT 188
                                                                  161 9J-----CG 181
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121
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US-09-896-791B-2 (1-1100) x US-09-864-761-41589 (1-53)
                                                                                                                                                                                   Sequence 112, Application US/09800729
Patent No. US20020068319A1
GENERAL INFORMATION:
TITLE OF INVENTION: 32 Human secreted proteins
FILE REFERENCE: P2044P1
CURRENT APPLICATION NUMBER: US/09/800,729
CURRENT PILING DATE: 2001-03-08
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR APPLICATION NUMBER: PCT/US00/26013
PRIOR APPLICATION NUMBER: 60/155,709
PROR FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 217
SOFTWARE: Patentin Ver. 2.0
SSEQ ID 0.112
LENGTH: 530
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Mismatches:
Indels:
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Matches:
                                                                                                                  GCCTCCATCATGCGCCTCACAATCAGCTAC 207
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144.50
29.678
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FEATURE:
NAME/KEY: SITE
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US-09-800-729-112
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LOCATION: (505)
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                                                                                                                                                                                                                                                                                     120 rpGluGlnLeuProSerTyrTyrPheAspTyrTrpGlyGlnGlyThrLeuValThrValS 140
                                                                                                                                                                                                                                                                                                                                              333 CGGAAAATGTCAGCAAGCACCTGGGCCTCAGTCAGTGGACCTCTGTTCCTCCTCCTCGTGAT 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 393 ACATAACCCCACTCCTGGTACCAATTTCTCTGGAGCTCATTGGACACAGTATCTTTGA 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 TICCCTGCGAATGAAGAGCACGCTCACCAGCAGAGGGCGCACGCTCAACCTCAAAGCGGC 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             273 roAlaLeuGluAspLeuLeuGlySerGluAlaAsnLeuThrCysThrLeuThrGlyL 293
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                                                                                                                                                                                                                            275 -- AAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATGGCTTACCTGT
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                                                                                                               CGCAGCAGGTGGAAAAAGGGGGAGAGCCACTGGACGCCTGCTACCTG------
                                                                                                                                                                                                                                                                                                                                                                                                 ...-SerAlaSerPro-----
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875 AAGGGACTGAATCCTCTCTCCCTCATGGGTGTTGTGGGCCCTTAACCGGAAAA 928 :::::	ATTGTCCTGGCTAGGAGGAGTGAAGGACATGGCCCAGCTATCC 97	972	1004 CCACCATAAAGACCTCTCCTTGT	euasn***LeuhisalaProProLysLysLysLysLysLysLysLysLysLysLysLysLysL	RESULT 14 US-09-764-868-850 US-09-764-868-850 Sequence 850, Application US/09764868 Patent No. US20020168711A1 GENERAL INFORMATION: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PT23 CURRENT APPLICATION NUBBER: US/09/764,868 CURRENT FILING DATE: 2001-01-17 Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510 SOFTWARE: PatentIn Ver. 2.0 LENGTH: 399 LENGTH: 399 TYPE: PRT	Alignment Scores: 0.00415 Length: 399 Pred. No.: 134.00 Matches: 108 Score: 36.80% Conservative: 37 Best Local Similarity: 27.41% Mismatches: 151 Query Match: 6.67% Gaps: 23	-896-7918-2 (1-1100) x US-09-764-86 9 CACGAGGGCCATGGCGTTGGGGCTGCAGCG	 HisArgGlyValGlnArgGluThrValHisArgAspGlySerGly	69 GAAGTCGCGGGACGCGCCCCAGCCGCGCAGCCAGGAGACGAGGTGCT 119 	120 GTACCAGCTGGCGACACTCTGCCCGTCGGCGTCAGCGCGCACCTGGA 173 	174 CAAGGCCTCCATCATGCGCCTCACAATCAGCTA
Qy Db	oy ob	A & A	• 6 6 6	7 da 65 da	RESULUS-09 No. 10 No. 1	Alignm Pred. Score: Percen Best L Query DB:	US-09	QQ	Oy Dp	Oy Db	Qy Dp

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979 ----CAGAAACCCACAAATGTCTCCAAAACCACCATAAAGACCTCTTCTTAGGCACC 1034
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| 154 OGlu-------HisHisLeuLeuArgLeuSerArgLeuArgValThrAr 168
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GCACCGCCTCTGCGCAGCAGGTGGAAA---AAGGGGGAGAGCCACTGGACGCCTGCTACC 272
                                      135 AlaProArgGlnAlaHisArgLeuArgLeuArgProProGlyProTrpLeuProArg-Pr 154
                                                                                                                                                                                          211 oGluThrArgArgAlaLeuProArgArgProArg---AlaValArgAlaLeuGlnGlyPr 230
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                                                                               273 TGAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATGGCTTACCTGT
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----AlaLeuArgArgLeuGlyHiSArg-------ArgProAlaProAlaPr
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----AGGATTCAGTCCCTTTCCCCTGTAGCACCTGAACAGGCCACCTCTTGACAAGACA 835
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| 133 aLeuGlyAlaValArgAlaGlyValGlyProLeuAlaArgValArgAlaLeuValLeuG1 153
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CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 1792
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 953
LENGTH: 200
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Matches:
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132.50
37.33%
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CORGANISM: Homo sapiens
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Search completed: December 2, 2002, 20:52:57 Job time: 48 secs

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us-09-896-791b-2.rpr

aryl hydrocarbon r cyclin r - fruit f protein C4167,5 [1]

aryl hydrocarbon

hypothetical prote brain and muscle A tegument protein 6 neurogenesis regul glucocorticoid rec probable large Pro brain and muscle A

cell proliferation hypothetical 70k p ORF2 protein - Orf eyelid - fruit fly

unconventional myo proline-rich prote probable proline-r

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C; Species: Homo sapiens (man)
C; Species: Homo sapiens (man)
C; Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
C; Accession: JC7771
R; Hara, S.; Hamada, J.; Kobayashi, C.; Kondo, Y.; Imura, N.
Biochem. Biophys. Res. Commun. 287, 808-813, 2001
A; Title: Expression and characterization of hypoxia-inducible factor (HIF)-3alpha in A; Reference number: JC7771; PMID:11573933
A; Contents: Kidney
A; Contents: Kidney
A; Contents: Man
A; Residues: 1-667 *HARA
A; Residues: 1-667 *HARA
A; Residues: 1-667 *HARA
C; Comment: This protein is a heterodimeric transcription factor that belongs to the b lved in the regulation of hypoxia-inducible gene expression in human kidney.
C; Genetics:
A; Gene: hif-3alpha
A; Map position: 19
C; Keywords: kidney
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-MODEL-frame+n2P; model 'DEV-x1P
-MODEL-frame+n2P; model 'DEV-x1P
-MODEL-frame+n2P; model 'DEV-x1P
-MODEL-frame+n2P; model 'DEV-x1P
-DB-PIR, 73 -QFMT-fastan -SUFFIX-rPr -MINMATCH-0.1 -LOOPCL-0 -LOOPEXT=0
-UNITS-bits -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-UNITS-bits -START=1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-UNCALIGN-200 -THE_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN-15 -MODE-LOCAL
-UNCALIGN-200 -THE_SCORE-pct -THR_MAX=100 -THR_MIN-0 -MAXIEN-2000000000
-USER-USO9965791 (GCM.1_1.30_@frund.LO112002.152658_5606 -NCPU-6 -ICPU-3
-NO_XIPXY -NO_MMAP -LARGEQUERY -NEG_SCORES-0 -WAIT -LONGIOG -DEV_TIMBOUT-120
-WARN_TIMEOUT-30 -THRRANS=1 -XGAPEXT=0.5 -FGAPOP-6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP-6 -DELEXT=7
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                    GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd

    protein search, using frame_plus_n2p model

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DB: 3 US-09-896-791B-2 (1-1100) x JC4837 (1-810) Qy	OY 109 ACGGAGGTGCTGTACCAGCTGCGCACACTCTGCGCGGGGGGGG	Qy 229 GCAGCAGGTGGAAAAAGGGGGGAGAG	Db 81 uLysAlaLeuAspGlyPheValMetValLeuThrAspAspGlyAspMetValTyrIIeSe 101 Oy 334 GGAAAATGTCAGCAAGCACCTCGGCCTCAGTGGACCTCTGTTCCTCCTCCTGATA 393 L::: ::: ::: ::: ::	Db 113	Oy 514 TCAAAGAAGCACTGGAAGCCCCAACAGAGCGCCACTTTCCCTGCGAATGAAGACACG 573 1	Qy 634 TCAGGACATATGAGGCCTACAAGCCCCTGCACAGACTTCCCTGCCGGAGCCCTGC 693 ::: :::	RESULT 3 JC7619 hypoxia-inducible factor 1 alpha - chicken C;Species: Gallus gallus (chicken) C;Becies: Gallus gallus (chicken) C;Becies: Gallus gallus (chicken) C;Becies: Gallus gallus (chicken) C;Becies: Gallus gallus (chicken) C;Accession: JC7619 R;Takahashi, T.; Sugishita, Y.; Nojiri, T.; Shimizu, T.; Yao, A.; Kinugawa, K.; Harad Biochem. Biophys. Res. Commun. 281, 1057-1062, 2001 A;Title: Cloning of hypoxia-inducible factor 1 alpha cDNA from chick embryonic ventri A;Accession: JC7619, MUID:21134360; PMID:11237772 A;Accession: JC7619 A;Accession: JC7619 A;Accession: JC7619 A;Accession: JC7619 A;Accession: JC7619 A;Accession: JC7619	A.Cross-references: DDB.AB013746 C.Comment: This factor belongs to the basic helix-loop-helix-Per/ARNT/Sim (HLH-PAS) f costsals of cells, and in redox stimuli. C.Genetics: A.Gene: hif-lalpha C.Keywords: embryo: transcription factor F:106-156/Domain: Per/ARNT/Sim, ligand binding, dimerization #status predicted <pasi></pasi>
Db 27 GlnGluThrGluValLeuTyrGlnLeuAlaHisThrLeuProPheAlaArgGlyValSer 46 Qy 163 GCGCACCTGGACAAGGCCTCCACAATCAGCTACCTGCGCATGCACGC 222	Db 67 LeuCysAlaAlaGlyGluTrpAsnGlnValGly AlaGlyGlyGluProLeuAspAlaCy 86 Qy · 268 CTACCTGAAGGCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGACATGGCTTA 327	. 106 rLeuSerGluAsnValSerLysHisLeuGlyLeuSerGln	OY 448 TTTGATTTATCCATCACCAAGAGGAACTTCAAGACGCCCCAGCCCC 507	Qy 568 AGCACGCTCACCAGCAGGGGGCGCACCTCAACCTCAAAGCGGCCACCTGGAAGGTGCTG 627	Db 188 AsnCysSerGlyHisMetArgAlaTyrLysProProAlaGlnThrSerProAlaGlySer 207 Qy 688 CCTGGCTCCGAGCCTCCCTGGAATGCCTGGTGTTATCTGTGAAGCCATCCCCCAGCTC 747 Db 208 ProAspSerGluProProLeuGlnCysLeuValLeuIleCysGluAlaIlePro 225 Qy 748 CCCTTCCACGATGGTGT 765	Db 226HisProGlySer 229 RESULT 2 JC4837 Hypoxia-inducible factor 1 alpha - mouse C; Species: Mus musculus (house mouse) C; Date: 15-Aug-1996 #sequence_revision 15-Oct-1996 #text_change 21-Jul-2000	C; Accession: JC4837 R; Wenger, R.H.; Rolfs, A.; Marti, H.H.; Guenet, J.L.; Gassmann, M. B; Wenger, R.H.; Rolfs, A.; Marti, H.H.; Guenet, J.L.; Gassmann, M. Biochem. Blophys. Res. Commun. 223, 54-59, 1996 A; Title: Nucleotide sequence, chromosomal assignment and mRNA expression of mouse hypoxi A; Reference number: JC4837; MUID:96254028; PMID:8660378 A; Rolecule type: mRNA A; Residues: 1-810 cWENA A; Residues: 1-810 cWENA A; Residues: 1-810 cWENA A; Cross-references: EMBL.X95580; NID:91430864; PIDN:CAA64833.1; PID:94379202 C; Comment: This factor is involved in the oxygen-regulated transcription of several gene C; Genetics: A; Genetics: A; Genetics: C; Keywords: transcription factor C; Keywords: transcription factor C; Keywords: transcription factor C; Scheckins: helix-loon-helix #status predicted	Alignment Scores: Pred. No.: 7.84e-41 Length: 810 Score: 610.50 Matches: 129 Percent Similarity: 67.65% Conservative: 32 Best Local Similarity: 54.20% Mismatches: 49 Query Match: 30.37% Indels: 28

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A;Cross-references: EMBL:U29165; NID:g1144012; PIDN:AAC51210.1; PID:g1144013
C;Genetics:
                                      A; Residues: 1-826 <RES>
A; Cross-references: EMBL:U22431; NID:g881345; PIDN:AAC50152.1; PID:g881346
A; Cross-references: EMBL:U22431; NID:g881345; PIDN:AAC50152.1; PID:g881346
A; Note: parts of this sequence were confirmed by peptide sequencing
R; Hogenesch, J.B.; Chan, W.K.; Carver, L.A.; Bradfield, C.A.
submitted to the EMBL Data Library, June 1995
A; Reference number: H00692
A; Reference number: H00692
A; Reference number: translated from GB/EMBL/DDBJ
A; Rolecule type: mRNA
A; Residues: 1-826 <H0G>
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ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
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A; Map position: 14q21-14q24
C; Keywords: heterodimer
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Best Local Similarity:
Query Match:
              preliminary
                           A; Molecule type: mRNA
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N:Alternate names: ARNT interacting protein
C:Species: Homo sapiens (man)
C:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 05-Nov-1999
C;Accession: 138972; G01875
C;Accession: I38972; G01875
C;Accession: I38972; G01875
A; Wang, G.L.; Jiang, B.H.; Rue, B.A.; Semenza, G.L.
Proc. Natl. Acad. Sci. U.S.A. 92, 5510-5514, 1995
A;Title: Hypoxia inducible factor 1 is a basic-helix-loop-helix-PAS heterodimer regulate
A;Reference number: 138972; MUID:95296340; PMID:7539918
 Per/ARNT/Sim, ligand binding, dimerization #status predicted <PAS2> conserved carboxy-terminal transactivation element #status predicted < conserved dileucine repeat, important for oxygen-dependent degradation
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Conservative:
Mismatches:
Indels:
Gaps:
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                                                              1.36e-40
607.50
67.36%
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30.22%
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                                                                                        Percent Similarity:
F;249-299/Domain:
F;762-811/Domain:
F;767-768/Region:
                                                     Aliqnment Scores:
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Uctobal Appoxia inducible factor 1 alpha homolog - fruit fly (Drosophila melanogaster) Uctobate: Drosophila melanogaster C; Species: Drosophila melanogaster C; Species: Drosophila melanogaster C; Species: Drosophila melanogaster C; Accession: JC4851
R; Nambu, J.R.; Chen, W.; Hu, S.; Crews, S.T.
Gene 172, 249-254, 1996
A; Title: The Drosophila melanogaster similar bHLH-PAS gene encodes a protein reliance number: JC4851
A; Reference number: JC4851
A; Reference number: JC4851
A; Molecule type: mRNA
A; MRNA
A; Molecule type: M
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c; comment: This protein associates to the aryl hydrocarbon receptor nuclear translocator
as erythropoietin, vascular endothelial growth factor, the GLUT1 glucose transporter, e
F;6-144/Region: basic helix-loop-helix #status predicted
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                                                                                                                               Pypoxia-inducible factor 1 alpha - rat
C;Species: Ratus norvegicus (Norway rat)
C;Species: Ratus norvegicus (Norway rat)
C;Accession: JC5809
R;Ladoux, A.; Frelin, C.
Biochem. Blophys. Res. Commun. 240, 552-556, 1997
A;Title: Cardiac expressions of HIF-1 alpha and HLF/EPAS, two basic loop helix/PAS of A;Reference number: JC5809; MUID:98063274; PMID:9398602
A;Accession: JC5809
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
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Db 210 Qy 483		A; Residues: 1-58 <res> A; Cross-references: GB:D44444; NID:g1088450; PIDN:BAA07906.1; PID:g1088451 A; Accession: 178524 A; Status: preliminary; translated from GB/EMBL/DDBJ</res>
	eLysGluAlaLeuSerLeuLysArgGluLeuAlaGlnLysValLysAspGluProGlnGl	A; Malecule Lype: DNA A; Residues: 117-152 < RE2> A; Cross-references: GB:D44446; NID:g1088454; PIDN:BAA07908.1; PID:g1088455
UY 54	543	A; Accession: I'8523 A; Status: preliminary; translated from GB/EMBL/DDBJ A; Molecule type: DNA
0y 57	CAGCAGAGGGGGCACCGCTCAACCTCAAGGCGCCACCTGGAAGGTGCTGCACTGCAGG	A; Residues: 37-116 <re3> A; Cross-references: GB: D4445; NID:g1088452; PIDN:BAA07907.1; PID:g1088453 B: Delahar I M . Dahmane X V 7</re3>
	rSerArgGlyArgSerIleAsnIleLysSerAlaSerTyrLysValIleHisIleThrGl	submitted to the EMBL Data Library, February 1995 A; Description: Down syndrome critical region encodes a gene with homology to Drosaphi
0y 0b 28	bis Acarateagesceracaagescereagaetr	A; Reference number: S61256 A; Accession: S61256 A; Status: preliminary
Oy 68 Db 30	681 CGGGAGCCCTCGCTCCGCAGCCTGCAATGCCTGGTGTATCTGTGAAGCCATCCC 740	A;Molecule type: mkNA A;Residues: 87-116 A;Cross-references: EMBL:X84790; NID:g971469; PIDN:CAA59261.1; PID:g971470 C;Genetics:
	CCAGCTCCCCTFCCACGATGGTGCTACTCTGGGTCTTCCACAGGAGAAGACTCCCATCTC	A;Gene: hSIM2 F;1-50/Region: helix-loop-helix #status predicted
Db 32 Oy 80	326SerLeuAspMetArgPheThrTyrValAspAspLysMetHisAspLeuLeuGly 343 801 TACCTTATTCACCCCTCTTTGGAAGGCACTACTTGTCTAGAAGGTGGCCTGTTCA 860	6 Length: Matches:
		larity: 53.77% imilarity: 38.21%
Oy 86 Db 36	861 GGTGCTACAGGGGAAAGGGACTGAATCCTCTCCCCTCATGGGTGTTGTGGGCCCTTAA 920	Gaps: Gaps: 520 (1-248)
0y 92		64
Db 37	378 GlnGlyGluThrSerArgTyrArgPheLeuGlyLysTyrGlyGlyTyrCysTrp1leLeu 397	Db 2 LysGluLysSerLysAsnalaalaLysThrArgArgGluLysGluAsnGlyGluPheTyr 21
Oy 97 Db 39	972 995 	Qy 124 CAGCTGGCGCACTCTGCGCGCGCGCGCGCGCGCGCCTGGACAAGGCCTCC 183 :::
Qy 99 Db 41	996TTAGGC 1031	Qy 184 ATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTGCGCAGGT 237
Qy 1032 Db 438	ACCAGAGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	QY 238GGAAAAAGGGGGACACCC
RESULT 7 A58520 single-m	ninded gene 2 protein - human (fragment)	QY 262 CGCCTGCTACCTGAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGACAT 321
C; Speci(C; Date: C; Acces: R; Osoega	C:Species: Homo sapiens (man) C:Date: 20-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 01-Dec-2000 C:Accession: A58520; I58111; I78524; I78523; S61256 R:Osoegawa, K.; Okano, S.; Kato, Y.; Nishimura, Y.; Soeda, E.	Qy 322 GGCTTACCTGTCGGAAAATGTCAGCAACCTGGGCCTCAGTCAG
DNA Res A;Title A;Refere A;Access	. 3, 175-179, 1996 : A 19-kb CpG island associated with single-minded gene 2 in Down syndrome chromc nore number: A58520; MUID:97061206; PMID:8905236	OY 382 TCCTCCCTGATACATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGACAC 441 Db 117
A; Statu: A; Molec: A; Resid: A; Cross-		OY 442 AGTATCTTTGATTTTATCCATCCTGTGACCAGGGAACTTCAAGACGCCCTGACCCC 501
R;Chen, Nature (A;Title: A;Refere	R;Chen, H.; Chrast, R.; Rossier, C.; Gos, A.; Antonarakis, S.E.; Kudoh, J.; Yamaki, A.; Nature Genet. 10, 9-10, 1995 A;Title: Single-minded and Down syndrome? [letter]. A;Reference number: I58111; MUID:95375794; PMID:7647800	Qy 502 AGGCCGAACCTGTCAAAGAAGCTGGAAGCCCCAACAGAGGGCCACTTTTCCCTG 558
A;Accession A;Status: p A;Molecule	A:Accession: I58111 A:Status: preliminary; translated from GB/EMBL/DDBJ A:Molecule type: DNA	QY 559 CGAATGAAGAGCACGCTCACCAGCAGGCGCACGCTCAACCTCAAAGCGGCCACCTGG 618

Db 165 ThrPhePheLeuArgMetLysCysValLeuAlaLysArgAsnAlaGlyLeuThr 182 Qy 607 GCGCCACCTGGAAGGTGCTGCACTGCACATATGAGGCCCTACAAGCCCCTGCA 666 :::::! ::: :::	RESULT 9 T21943 hypothetical protein F38A6.3a - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T21943; T26899 R;Mortimore, B. submitted to the EMBL Data Library, March 1997 A;Reference number: 219491 A;Accession: T21943	A, Status: preliminary; translated from GB/EMBL/DDBJ A, Molecule type: DNA A, Residues: 1-823 < WIL.> A, Residues: 1-823 < WIL.> A, Cross-references: EMBL: 292833; PIDN: CAB07380.1; GSPDB: GN00023; CESP: F38A6.3a A, Experimental source: clone F38A6 R, Ainscough, R. Submitted to the EMBL Data Library, June 1998 A, Reference number: 220282 A, Accession: T26899 A, Status: preliminary; translated from GB/EMBL/DDBJ	A; Molecule type: DNA A; Residues: 1-823 < WIZ> A; Cross-references: EMBL:AL023842; PIDN:CAA19520.1; GSPDB:GN00023; CESP:F38A6.3a A; Experimental source: clone Y44A6D C; Genetics: A; Genetics: RSP:F38A6.3a A; Map position: 5 A; Introns: 19/2; 75/1; 111/2; 175/1; 226/3; 331/3; 518/1; 627/2; 711/1; 768/3	Alignment Scores: 2.55e-09 Length: 823 Pred. No.: 216.50 Matches: 69 Forcent Similarity: 47.334 Conservative: 46 Best Local Similarity: 28.40% Mismatches: 66 Query Match: 10.77% Indels: 63 DB: 2 Gaps: 9	US-09-896-791B-2 (1-1100) x T21943 (1-823) QY 43 AGGTCGAACACCGAGCTGCGGAAGGAAGTCGCGGGCCCGCAGCCGGCGCGCGC	::: ;:::::::: LysGluSerAspllePheAspAspLeuLysMetCysValProIleValGluGluGlyThr AGCGCGCACCTGGACAAGGCCTCCATCATGCGCTCACAATCAGCTACCTGCGCATGCAC ::::::::::::: :::	Qy 220 CGCCTCTGCGCAGCAGCAGAAAAGGGGGA
Db 163 ArgMetLysCysValLeuAlaLysArgAsnAlaGlyLeuThrCysSerGlyTyr 180 Qy 619 AAGGTGCTGCTCAGGACATATGAGG 648 ::	Cell 52, 143-151, 1988 A;Title: The Drosophila single-minded gene encodes a nuclear protein with sequence simil A;Title: The Drosophila single-minded gene encodes a nuclear protein with sequence simil A;Reference number: A29945; MUID:88151023; PMID:3345560 A;Accession: A29945 A;Accession: A29945 A;Accession: A29945 A;Residues: 1-655 <cre> A;Cross-references: GB:M19020; NID:g158464; PID:g158465 C;Genetics: A;Cross-references: FlyBase:FBgn0004666 C;Keywords: DNA binding: transcription regulation</cre>	Alignment Scores: 2.11e-11 Length: 655 Score: 242.50 Matches: 76 Percent Similarity: 45.56% Conservative: 42 Best Local Similarity: 29.34% Mismatches: 67 Query Match: 2.06% Indels: 74 DB: 2.06% Gaps: 7 US-09-896-791B-2 (1-1100) x A29945 (1-655)	CAGCTGGCCACACTCTGCCCTTTGCG :::	Qy 238	Oy 325 TTACCTGTCGGAAAATGTCAGCACCTCGGCCTCAGTCAGT	445 105 505	Db 125 ProHisIleAsnGlnHisProLeuAlaGlnThrHisThrProIleGlySerProAsnGly 144 Qy 529GAAGCCCAACA

us-09-896-791b-2.rpr

ογ	304 CACCGCCGAGGGAGACATGCCTGTCGGAAATGTCAGCAAGCA	qq	::
đ	: :::::: :::: ::: ::: ::: ::: :::	Qy	103 CAGGAGACGGAGGTGCTGTACCAGCTGGCGCACACTCTGCCCTTTGCGCGCGGCGTC 159
δō	364 TCAGIG-GACCTCTGTTCCTCCTCCTGATACATAACCCCACTCCTGGTACCAATTTCTC 422	qq	::: ::::::::::::::::::::::::::::::::
qa	225 rGlnThrAsp 228	Qy	160 AGCGCGCACCTGGACAAGGCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCAC 219
Qy	423 TCTGGAGCTCATTGGACACAGTATCTTTGATTTTATCCATCC	qq	
qa	229LeuThrGlyargAlaLeuArgAspPheLeuHisProSerAspTyrAspGluPh 246	δδ	
ογ	483 TCAAGACGCCTGACCCCCAGGCCGAACCTGTCAAAGAAGCTGGAAGCCCCCA 537	QΩ	::: ::: ::: 170 Lys-ThrAlaGlyAsnValLeuGluAsnAsnLeuAspAsnGluIleThrAsnGluValTr 189
qa	246 eAspLysGlnSerLysMetLeuHisLysProArgGl 258	ďδ	TACCTG
δō	538ACAGAGCGCCACTTTTCCCTGCGAATGAAGAGCACGCTCACCAG 581	qa	189 pThrGluAspThrIlealaGluCysLeuAspGlyPheValMetIleVa 205
qa	258 yGluAspThrAspThrThrGlyIleAsnMetValLeuArgMetLysThrValIleSerPr 278	Qy	304 CACCGCCGAGGGAGACATGGCTTACCTGTCGGAAAATGTCAGCAAGCA
δy	582 CAGAGGCCCACGCTCAACCTCAAAGCGGCCACCTGGAAGGTGCTGCA 629	qa	205 laspSerAspSerSerIleLeuTyrValThrGluSerValAlaMetTyrLeuGlyLeuTh 225
qa	 CysLeuAsnLeuLysSerAlaLeuTyrLysSerValSerPheLe	Qy	364 TCAGTG-GACCTCTGTTCCTCCTCGATACATAACCCCACTCCTGGTACCAATTTCTC 422
Qy	630 CTGCTCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCC 677	QΩ	225 rGlnThrAsp 228
đa	298 sserLysValSerThrGlyGlyHlsValSerPheMetGlnGlyIleThr1lePr 316	οy	423 TCTGGAGCTCATTGGACACAGTATCTTTGATTTTATCCATCC
Qy	678 TGCCGG 684	qa	
qa	316 oAlaGly 318	οy	483 TCAAGACGCCCTGACCCCCAGGCCGAACCTGTCAAAGAAGAAGAAGCTGGAAGCCCCA 537
R E	RESULT 10	QQ	346 e
hy C::	171194 171190thetical protein F38A6.3b - Caenorhabditis elegans C.Species: Caenorhabditis elegans	δλ	538ACAGAGGGCCACTTTTCCCTGCGAATGAGAGCACGCTCACAG 581
ΰΰ	C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C:Accession: T21944; T26900	qa	258 yGluAspThrAspThrThrGly1leAsnMetValLeuArgMetLysThrVallleSerPr 278
S S C	R;Mortimore, B. Wolmitted to the EMBL Data Library, March 1997	δο i	582 CAGAGGGCGCACGCTCAACCTCGAAGGGCCCACCTGGAAGGTGCTGCA 629
A A	A; Relefence number: 219491 A; Accession: T21944	<u>a</u>	
; A	A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA	δλ	CCCCTGCACAGACTTCCCC
A;(<pre>cesidues: 1-825 <wil> Loss-references: EMBL:292833; PIDN:CAB07381.1; GSPDB:GN00023; CESP:F38A6.3b</wil></pre>	අු	298 sSerLysValSerThrGlyGlyHisValSerPheMetGlnGlyIleThrIlePr 316
A 8		δy	678 TGCCGG 684
su	submitted to the EMBL Data Library, June 1998 A:Reference number: 220282	qq	316 oAlaGly 318
A	A:Accession: T26900 A:Status: preliminary: translated from GR/FMRL/DDRJ	RESU T242	RESULT 11
A A	A.Wolecule type: DNA A.Residnes: 1-825 <wi>></wi>	odkų	
A;	A;Cross references: EMBL:AL023842; PIDN:CAA19521.1; GSPDB:GN00023; CESP:F38A6.3b A;Experimental source: clone Y44A6D	C; Da	ie: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 15-Oct-1999 pession: T24292
ઇં &ેં	C; Genetics: A; Gene: CESP: F38A6.3b	R;St subm	wward, C. Itted to the EMBL Data Library, October 1996
A	A;Map position: 5 A;Introns: 19/2; 75/1; 111/2; 175/1; 226/3; 331/3; 518/1; 627/2; 713/1; 770/3	A; Re A; AO	ference number: 219870 Session: T24292
Al	mment Scores:	A;St A;Mo	ntus: preliminary; translated from GB/EMBL/DDBJ Lecule type: DNA
Scor	. No.: 2.55e-09 Length: 2.55e-09 Matches:	A; Re	sidues: 1-300 <mil> oss-references: EMBL:281110; PIDN:CAB03258.1; GSPDB:GN00023; CESP:T01D3.</mil>
	Described Similarity: 28.40% Mismatches: 66 Ouery Match: 28.40% Mismatches: 63 Ouery Match: 2 Gaps: 9	A; Ge	A;Experimental source: clone Tolds C;Genetics: A;Gene: CESP:TOlD3.2 A:Map position: 5
Sn		A; In	A;Introns: 69/3; 121/3
Qy	43 AGGTCGAACACCGAGCTGCGGAAGGAGAAGTCGCGGGGGGGG	Alig Pred	Alignment Scores: 8.24e-06 Length: 300

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.B03258.1; GSPDB:GN00023; CESP:T01D3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                            GAAGGCCCTGGAGGGTTTCGTCATGGTACT 303
|||:::|||||||||||::::
-----LeuAspGlyPheValMetIleVa 205
                                                                                                                                                                                                                                                                                                                          GGAAAATGTCAGCAAGCACCTGGGCCTCAG 363 :||||:::|||:::
irGluServalAlaMetTyrLeuGlyLeuTh 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VTTTATCCATCCCTGTGACCAAGAGGAACT 482
|||||:::|||||| ||| :::|||
ipPheLeuHisProSerAspTyrAspGluPh 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTCCCTGCGAATGAAGAGCACGCTCACCAG 581
||||||||||||||:: :::::
tValLeuArgMetLysThrValIleSerPr 278
                             :::|||
MetCysValProIleValGluGluGlyThr 149
                                                                               CGCCTCACAATCAGCTACCTGCGCATGCAC 219
                                                                                                        ||||:::
|ArgValAlaAlaThrIleCysArgLeuArg 169
                                                                                                                                                                                                                                                                                                                                                                                                         ACATAACCCCACTCCTGGTACCAATTTCTC 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CACACTCTGCCCTTTGCG----CGCGGCGTC 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTCAAAGAAGAAGCTGGAAGCCCCA---- 537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACCTGGAAG------GTGCTGCA 629
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | :::|||
|aLeuTyrLysSerValSerPheLeuValHi 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nLeuAspAsnGluIleThrAsnGluValTr 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCCTACAAGCCCCCTGCACAGACTTCCCC 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.24e-06
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Score: 166.50 Matches: 62 Percent Similarity: 40.43\$ Conservative: 50 Best Local Similarity: 22.38\$ Mismatches: 83 Query Match: 2.88\$ Indels: 83 DB: 209-896-791B-2 (1-1100) x JC7633 (1-392)	64 AAGGAAAGTGGGGACGGCCC ::: ::: 47 ArgGluAsnHisSerGluIleGluA	Qy 124 CAGCTGGCGCACACTCTGCGCGGGGGGGCGCGCGCGCGCG	Qy 184 ATCATGCGCCTCACAATCAGCTACCTGCGCATGCGCCCTCTGCGCAGCAGCAGGAAAA 243	Oy 244 AGGGGAGAGCCACTGGACCCTGCTAC	Oy 272CTGAAGGCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGA 318	Oy 319 CATGGCTTACCTGTCGGAAATGTCAGCAAGCACCTGGGCCTCAGTCAGTGGACCT 374 ::: ::: :::: ::: :: Db 141 gVallleTyrValSerAspSerValThrProValLeuAsnHisProGlnSer 158	QY 375 CIGITCCTCCTCCTGATACATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCAT 434	QY 435 TGGACACAGTATCTTTGATTTTATCCATGACCAAGAGGAACTTCAAGACGCCT 494 ::::: ::: ::	OY 495 GACCCCAGGCCGAACCTGTCAAAGAAGCTG	Qy 528 528 Db 201 sLysGluGlyGlnGlnSerSerMetArgMetCysMetGlySerArgArgSerPheileCy 221	Oy 529GAAGCCCCAACAGAGCGCCACTTTCCCTGCGAATGAAGAGCAC 572	Oy 573 GCTCACCAGCAGGGCGCACGCTCAACCTCAAAGGGGCCACCTGGAA 620 ::::	Oy 679 -GCCGGGAGCCCTCGCAGCCTCCCCTGCAATGCCTGGTGCTTATC 726 ::: Db 280 pGluaspThrGlualaGlyGlnThrSerLySTyrCysLeuValalaIle 296	RESULT 13 JC7635 aryl hydrocarbon receptor nuclear translocator 1 - chicken N.Alternate names: hypoxia-inducible factor 1 beta C;Species: Gallus gallus (chicken) C;Species: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001	C;Accession: UC/035 R;Catron, T.; Mendiola, M.A.; Smith, S.M.; Born, J.; Walker, M.K. Biochem. Biophys. Res. Commun. 282, 602-607, 2001
Score: 172.50 Matches: 59 Percent Similarity: 46.82% Conservative: 44 Best Local Similarity: 26.82% Mismatches: 70 Query Match: 2.858% Indels: 47 DB: 2 Gaps: 6 US-09-896-791B-2 (1-1100) x T24292 (1-300)	SCGCACACTCTGCCCTTTG ::: AlaAsnGluLeuProLeuA	OY 181 TCCATCATGCGCCTCACAATCAGCTACGGCATGCACCGCTCTGCGCAGCAGGTGGA 240 :::::::: :: ::	Oy 241 AAAAGGGGAGAGCCCACTGGACGCCTGCTAC	Oy 272 -CTGAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCGAGGGAAGACATGGCTTACCT 330	Oy 331 GTCGGAAAATGTCAGCAAGCACCTGGGCCTCAGTGGACCTCTGTTCCTCCTCCTG 390 : ::: :::	OY 391 ATACATAACCCCACTCCTGGTACCAATTTCTCTGGAGCTCATTGGACACAGTATCTT 450 Db 100	OY 451 GATTTTATCCATCCTGTGACCAGGGAACTTCAAGACGCCCTGACCCCCAGGCCGAAC 510	OY 511 CTGTCAAAGAAGGAGGCCCCAACAGAGGGCCCCTTTCCCTGCGAATGAAGAG 570 Db 124ASnTyrCysAspLeuAsnTrpProGlnMetCysAsnValArgValLysSer 140	Qy 571 ACGCTCACCAGCAGGGCGCACGCTCAAACCGGCCACCTGGAAGGTGCTG 627 :::	Oy 628 CACTGCTCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACT 672	Oy 673 TCCCTGCCGGGAGCCCTCGCAGCCTCCCTGCAATGCCTGGTGCTTA 724 :	RESULT 12 JC7633 aryl hydrocarbon nuclear translocator ARNT2-like factor, ARNT2X - zebra fish C;Species: Brachydanio rerio (zebra fish) C;Date: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 30-Jun-2001 C;Accession: JC7633 R;Buy, H.J.; Wangy, W.D.; Huy, C.H. Biochem Bi	A;Title: Ectopic expression of negative ARMT2 factor disrupts fish development. A;Title: Ectopic expression of negative ARMT2 factor disrupts fish development. A;Reference number: JC7633; MUD:21294759; PMID:11401485 A;Contents: Heart A;Accession: JC7633	A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-392 <hsu> A; Cross-references: GB:AY007992 C; Comment: This factor, a basic helix-loop-helix PAS (bHLH-PAS) factor, heterodimerizes C; Genetics: A; Gene: arnt2X</hsu>	Alignment Scores: Pred. No.: 2.5e-05 Length: 392

A) Re P) Re P) Ro C) CO C) CO C) Ge C) Ge C) Ge	A; Reference number: JC7635; MUID:21294777; PMID:11401503 A; Contents: Embryo A; Accession: JC7635 A; Molecule type: mRNA A; Residues: J-805 < CAP> C; Comment: This protein, known as hypoxia-inducible factor 1 beta, a member of the basic ponses to hormonal and environmental stimuli. It is also a common dimer partner for tran C; Genetics: A; Genetics: A; Gene: arntl C; Keywords: transcription factor	QY 622
Alignm Pred. Score: Percen Best L Query DB:	Alignment Scores: Pred. No.: 162.00 Matches: Score: 162.00 Matches: 66 Percent Similarity: 36.25\$ Conservative: 46 Best Local Similarity: 21.36\$ Mismatches: 76 Gaps: 9	RESULT 14 A56241 aryl hydrocarbon receptor nuclear translocator protein - mouse C; Species: Mus musculus (house mouse) C;Date: 03-0ct-1995 #sequence_revision 03-0ct-1995 #text_change 05-Nov-1999 C;Accession: A56241
us-09 Qy Db	9-896-791B-2 (1-1100) x JC7635 (1-805) 58 CTGCGGAAGGAAGATCGCGGGACCGGCCCGCGCGCGCGCG	R; Reisz-Porszasz, S.; Probst, M.R.; Fukunaga, B.N.; Hankinson, O. Mol. Cell. Biol. 14, 6075-6086, 1994 A;Title: Identification of functional domains of the aryl hydrocarbon receptor nuclea A; Reference number: A56241; MUID:94344118; PMID:8065341 A; Accession: A56241 A; Status: preliminary
oy oy	118 CTGTACCAGCTGCGCACACTCTGCGCGGGGGGGCGCGCACCTGGACAG	A:Wolecule type: mRNA A:Residues: 1-791 <rei. (rei.)="" 1-791="" 375="" 380="" 507="" <rei.="" a:cross="" a:gene:="" a:note:="" a:residues:="" arnt<="" as="" authors="" c:genetics:="" cag="" codon="" failed="" for="" gb:u10325;="" gln="" nid:9555687;="" pid:9555688="" pidn:aaa56717.1;="" references:="" residue="" ser,="" tgt="" th="" the="" to="" translate="" translated="" ttt=""></rei.>
d vy	129 LeuThrIleLeuArgMetAlaValSerHisMetLysSerLeuArg 143 238 GGAAAAAGGGGAGGCCCCTGGAGGCCTCCTAC	Alignment Scores: 0.000111 Length: 791 Pred. No.: 0.000111 Length: 791 Score: Score: 158.50 Matches: 63 Percent Similarity: 41.73% Conservative: 53 Past Loval Similarity: 22.66% Mismatches: 82
Oy Dp		7.89% Indels: 2 Gaps: 100) x A56241 (1-791)
s B &	-GGAGACATGGCTTACCTGTCGGAAATGTCACCAGCACCTGGGCCTCAGTCAGTCTCAGTCAGTCTCAGTCAGTCTCAGTCAGTCTCAGTCAGT	Qy 58 CTGCGGAAGGAGAAGTCGCGGGACCCGCGCCGCGCGCGCG
à 8 5	203G1 203G1 203	<pre>Qy 118 CTGTACCAGGTGGCGCACACTCTGCCGTTTGGGGGGGGGG</pre>
6° B		<pre>Qy 178 GCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCCACCGCCTCTGCGCAGCAGGT 237</pre>
3 B 3	CONTROLL MANAGEMENT	Qy 238 GGAAAAAGGGGAGACCACTGGACGCCTGCTAC
ଟ ପ ଓ	nLysAspProAlaAlaProProGluSerAl	Qy 272
8 6 6	5/9 CAGGAGGGGCAGGCTCAACCTCAAAGGGGCCACCTGAAGG	<pre>Qy 314 -GGAGACATGGCTTACCTGTCGGAAAATGTCAGCACGCTGGGCCTCAGTCAGT 368</pre>
ි සි		Qy 369 GGACCTCTGTTCCTCCTGATACATAACCCCACTCCTGGTACCAATTTCTCTCTGGA 428 1 Db 203
Oy Dp	621	Qy 429 GCTCATTGGACACAGTATCTTTGATTTTATCCATCCCTGTGACCAAGAGGAACTTCAAGA 488

	OY 309 CCGGGGGAGACATGCCTTACCTGTCGGAAATGTCAGCAACACCTGGGCCTCAGTC OY 309 CCGGGGGAGACATGCCTTACCTGTCGGAAATGTCAGCAACACCTGGGCCTCAGTC I		Oy 546 Db 245 Oy 585 Oy 636 Oy 636 Db 302 Oy 729 Db 341 Oy 757 Db 341 Oy 801 Db 361 Search com
203 uTrpPheGlySerThrLeuTyrAspGlnValHisProAspAspValAspLysLeuArgGl 489 CGCCTGACCCCCAGGCGAACCTGTCAAAGAAGCTGGAAGCCCCAACA :	Db 243 rValLysLysGluGlyGlnGlnSerSerMetArgMetCysMetGlySerArgArgSerPh 263 Oy 552 TTCCTGCGAATGAAGAGACCCTCACCAGC	618 GAAGGTGCTGCACTCGCACATATGAGGGCCTACAAGCCCCTGCACAGACTTCCCC	UC5405 Drain and muscle Ah receptor nuclear translocator-like protein, BMALIb - human C.Species: Homo sapiens (man) Bi.Chem. 10-Jun.1997 A.Title: CORNA cloning and tissue-specific expression of a novel basic helix-loop-helix/p A.Title: Usage. A.Title: Loud coning and tissue-specific expression of a novel basic helix-loop-helix/p A.Title: Usage. A. Recession: UC5405 A.Status: nucleic acid sequence not shown A.Ricatus: nucleic acid sequence not shown A.Ricatus: nucleic acid sequence not shown A.Ricatus: nucleic acid sequence not shown A.Micross: references: DBBJ:AB000812; NID:92094734; PIDN:BAA19935.1; PID:92094735 A.A.Coss: nucleic acid sequence not shown A.Micross: nucleic acid sequence not shown A.Micro

Perfect score:

Sequence:

OM nucleic

Run on:

Scoring table:

Total number

Searched:

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P30561 mus musculu
P41738 rattus norv
096433 drosophila
008785 mus musculu
015545 drosophila
015516 homo sapien
015516 nomo sapien
P97460 mus musculu
0910772 homo sapien
061026 mus musculu
0900172 homo sapien
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rattus norv
 homo sapien
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wenger R.H., Rolfs A., Kvietikova I., Spielmann P., Zimmermann D.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene expression by hypoxia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIFA_MOUSE STANDARD; PRT; 822 AA.
601221, 605165; 061664; 008993; 008741;
01-NOV-1997 (Rel. 35, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypoxia-inductble factor 1 alpha (HIF-1 alpha) (ARNT interacting protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=129/SvJ;
MEDILNE=98034461; PubMed=9368100;
Luo G., Gu Y.-Z., Jain S., Chan W.K., Carr K.M., Hogenesch J.B.
Bradfield C.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Molecular characterization of the murine Hif-1 alpha locus."; Gene Expr. 6:287-299(1997).
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P54258
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                   002748
000327
P35869
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STRAIN=C57BL/6; TISSUE-Hepatocytes;
MEDLINE-96355491; PubMed-8702901;
Li H., Ko H.P., Whitlock J.P. Jr.;
"Induction of phosphoglycerate kinase 1
Roles of Arnt and HFFlalpha.";
                                                                                                           CCT_DROME
CLOC_MOUSE
ARNT_DROME
NCO2_HUMAN
CLOC_HUMAN
NPA2_MOUSE
NCO2_RAT
PRDD_HUMAN
DRPL_RAT
DRPL_RAT
NPA2_HUMAN
NCO2_XENLA
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MY15_HUMAN
Y215_ADE02
                   ARNT_RABIT
BMAL_HUMAN
AHR_HUMAN
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ELL2_HUMAN
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[2]
                                                                                               AHR_RAT
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MEDLINE=97354184; Pubmed=9210478;
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HIFA_MOUSE
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 -MODEL-frame+_n2p.model -DEV-xlp
-Q-CQR02_1/USPTO_spool/US0986591/runat_02122002_152658_5574/app_query.fasta_1.1287
-Q-CQR02_1/USPTO_spool/US0986591/runat_02122002_152658_5574/app_query.fasta_1.1287
-Q-CQR02_1/USPTO_spool/US0986591
-UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-PT-1 - MATRIX-blosum62 -TRANS-human40.cdi -LIST-45
-DOCALIGN-200 -THR_SCORE-PT-500 - MILEN-0 - ALIGEN-2000000000
-USPT-ptc -NORM-ext -HRAPSIZE-500 -MILEN-0 -MAXLEN-2000000000
-USFR-US09896791_@CGN_11_13_@cunat_02122002_152658_5574 -NCPU-6 -ICPU-3
-NOX_XLPXY -NO_MANP -LARGEDGRRY -NGC_SCORES-0 -WAIT -LONGIGG -DEV_TIMEOUT-120
-WARN TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7
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                   GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd

    protein search, using frame_plus_n2p model

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between the Swiss Institute of Bioinformatics and the EMBL outstation. The European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                             SIMILARITY).

SUBCELGULAR LOCATION: Nuclear (Potential).

TISSUE SPECIFICITY: UBIOUITOUS.

DOMAIN: BOTH HYPOXIA RESPONSIVENESS AND TRANSACTIVATION CAPABILITY RESIDE WITHIN THE C-TERMINAL PART.

FESTIDE WITHIN THE C-TERMINAL PART.

FIM: REQUIRES PHOSPHORYLATION FOR DNA-BINDING.

SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.

SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
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                                 Gassmann M.;
mRNA expression
             MEDLINE-96254028; Pubmed-8660378;
Wenger R. H., Rolfs A., Marti H.H., Guenet J.-L.,
"Nucleotide sequence, chromosomal assignment and
mouse hypoxia-inducible factor-1 alpha.";
                                                                               Biochem. Biophys. Res. Commun. 223:54-59(1996)
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EMBL, Y09085; CAA70306.1; --
EMBL, Y09085; CAA70306.1; --
EMBL, Y09085; CAA70306.1; --
EMBL, AF004141; AAC53461.1; --
EMBL, AF004141; AAC53461.1; JOINED.
EMBL, AF004142; AAC53461.1; JOINED.
EMBL, AF004144; AAC53461.1; JOINED.
EMBL, AF004145; AAC53461.1; JOINED.
EMBL, AF004145; AAC53461.1; JOINED.
EMBL, AF004149; AAC53461.1; JOINED.
EMBL, AF004149; AAC53461.1; JOINED.
EMBL, AF004189; AAC53461.1; JOINED.
EMBL, AF004159; AAC53461.1; JOINED.
EMBL, AF004152; AAC53461.1; JOINED.
EMBL, AF004153; AAC53461.1; JOINED.
EMBL, AF004153; AAC53461.1; JOINED.
EMBL, AF004153; AAC53461.1; JOINED.
EMBL, X05580; CAA64833.1; -
EMBL, X05580; CAA64833.1; -
EMBL, X05580; CAA64833.1; -
TRANSFAC; T04666; -
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InterPro; IPR001321; HypoxindFlA.
InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS_domain.
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SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS50038; HLH—1; 1.
PROSITE; PS50888; HLH—2; 1.
PROSITE; PS50112; PAS; 2.
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EMBL; AF003695; AAC53455.1; -
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Pfam; PF00989; PAS; 2.
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                                                                                                                                                                                                                                                                                                                                  94 CGGCGCAGCCAGGAGACGGAGGTGCTGTACCAGCTGGCGCACACTCTGCCCTTTGCGCGC 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ------Bhe--GluLeuAlaGly 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 CysGly-----TyrLysEysProProMetThrCysLeuValLeuIleCysGluProIle 227
                   BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
PAS 1.
PAS 2.
PAC.
                                                                                                                                                                                                                                                                                                                                                                                                     9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGGGAGCCCTCGCTCCGAGCCTCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATC
                                                                                                                                                                                                                                                                                                                                                                             CGAATGAAGAGCACGCTCACCAGCAGGGGGGCGCACGCTCAACCTCAAAGCGGCCACCTGG
                                                                                                                                                                                                                                                                                      34 CAGCGCGTGAGGTCGAACACCGAGCTGCGGAAGGAGAAGTCGCGGGACGCGCCCGCAGC
                                                                                                                                                                                                                                                                                                                                              29 ArgArgSerLysGluSerGluValPheTyrGluLeuAlaHisGlnLeuProLeuProHis
                                                                                                                                                                                                                                                                                                                                                                                                                           214 ATGCACCGCTCTGCGCAGCAGGTGGAAAAAGGGGGAGAG-------CCACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 69 ValArgLysLeuLeuAspAlaGlyGly-LeuAspSerGluAspGluMetLysAlaGlnMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      259 GGACGCCTGCTACCTGAAGGCCCTGGAGGTTTCGTCATGGTACTCACCGCCGAGGGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  379 TCCTCCTCCTGATACATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             439 CACAGTATCTTTGATTTTATCCATCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         499 CCCAGGCCGAACCTGTCAAAGAAGAAGCTGGAAGCCCCAACAGAGCGCCACTTTTCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       190 LysValLeuHisCysThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGln
Repeat; DNA-binding; Nuclear protein; Transcription regulation;
                                                                           S -> T (IN REF. 1).
A -> T (IN REF. 2 AND 3).
I -> L (IN REF. 1).
E -> ERLLQENVNTPNFSQ (IN REF. 2).
                                                                                                                        -> N (IN REF. 3 AND 4).
-> V (IN REF. 4).
E717ADCE4CA9D795 CRC64;
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129
35
31
51
28
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Mismatches:
Indels:
                                                                                                                                                                                            Matches:
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                                                                                                                                                                                                                                                                US-09-896-791B-2 (1-1100) x HIFA_MOUSE (1-822)
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           Activator; Phosphorylation.
                                                                                                                                                                               8.3e-36
613.50
67.49%
53.09%
30.52%
                                                                                                                                   785
91858 I
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128
351
511
686
785
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TRANSCRIPTION FACTORS.
-!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -i- DOMAIN: BOTH HYPOXIA RESPONSIVENESS AND TRANSACTIVATION CAPABILITY RESIDE WITHIN THE C-TERMINAL PART.
-i- PTM: REQUIRES PHOSPHORYLATION FOR DNA-BINDING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Hepatoma;
MEDLINE-97236817; PubMed-9079689;
Hogenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z.,
Hogenesch J.B., Perdew G.H., Bradfield C.A.;
Pray-Grant M., Perdew G.H., Bradfield C.A.;
Characterization of a subset of the basic-helix-loop-helix-PAS
superfamily that interacts with components of the dioxin signaling
                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                           01.MOV-1997 (Rel. 35, Last sequence update)
16-027-2001 (Rel. 40, Last annotration update)
Hypoxia-inducible factor 1 alpha (HIF-1 alpha) (ARNT interacting protein) (Member of PAS protein 1) (MOP1) (HIF1 alpha).
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., AND SEQUENCE OF 166-170; 259-289 AND 771-781. MEDLINE=95296340; PubMed=7539918; Mang G.L., Jiang B.-H., New E.A., Semenza G.L.; Hypoxia-inducible factor 1 is a basic-helix-loop-helix-PAS heterodimer regulated by cellular O2 tension.", Proc. Natl. Acad. Sci. U.S.A. 92:5510-5514(1995).
                                                                                                                                           826 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KIDNEY AND HEART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biol. Chem. 272:8581-8593(1997).
[3]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; U29165; AAC51210.1; -.
EMBL; AF207601; AAF20139.1; -.
EMBL; AF207602; AAF20149.1; -.
EMBL; AF208487; AAF20149.1; -.
                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
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                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRANSFAC; T01610; -.
Genew; HGNC:4910; HIF1A.
                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
                                            228 Pro 228
CCC 741
                                                                                                                                         HIFA_HUMAN
Q16665;
739
                                                                                                                  HIFA_HUMAN
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168
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              394 CATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGACACAGTATCTTTGAT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 AACACCGAGCTGCGGAAGGAGAAGTCGCGGGACGCGGCCCGCAGCCGGCGCGCAGGAG 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            274 GAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATGGCTTACCTGTC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGGCCGAACCTG 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        155 ValLysLysGlyLysGluGlnAsnThrGlnArgSerPhePheLeuArgMetLysCysThr 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
PAS 1.
PAS 2.
                                                                                 DR PÉAM; PF00785; PAC; 1.
DR PÉAM; PF00989; PAS; 2.
DR PÉAM; PR01089; PAS; 2.
DR PRINTS; PR01080; PAS; 2.
DR SMART; SM00383; HLM; 1.
DR SMART; SM00091; PAS; 2.
DR SMART; SM00091; PAS; 2.
DR PROSITE; PS00098; HLM=1; 1.
DR PROSITE; PS00098; HLM=2; 1.
DR PROSITE; PS00112; PAS; 2.
DR PROSITE; PAS; 2.
DR PROSITE; PS00112; PAS; 2.
DR PROSITE; PS00112; PAS; 2.
DR PROSITE; PAS; 2.
DR PROSITE; PAS; 2.
DR PROSITE; PAS; 2.
DR PRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CTGGACAAGGCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       514 TCAAAGAAGAAGCTGGAAGCCCCAACAGAGCGCCACTTTTCCCTGCGAATGAAGAGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCAGCAGGTGGAAAAAGGGGGAGAG----------CCACTGGACGCCTGCTACCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABD4F7DAA135BE2D CRC64;
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129
33
48
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Mismatches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLY-THR
InterPro; IPR001092; HLH_basic.
InterPro; IPR001321; HypoxindFlA.
InterPro; IPR001610; PAC.
InterPro; IPR0000014; PAS_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    92670 MW;
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606.50
68.07%
54.20%
30.17%
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298
345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AA;
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Best Local Similarity:
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85
228
302
615
826 $
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
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Mech. Dev. 63:51-60(1997).

-! FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE INDUCTION OF OXYGEN REGULATED GENES. SPECIFICALLY RECOGNIZES AN 8 BP HYPOXIA RESPONSE ELEMENT (HRE). REGULATES THE VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) EXPRESSION AND SEEMS TO BE IMPLICATED IN THE DEVELOPMENT OF BLOOD VESSELS AND THE TUBULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE IN THE FORMATION OF THE ENDOTHELUM GIVING RISE TO THE BLOOD BRAIN BARRIER. POTENT ACTIVATOR OF THE TIE-2 TYROSINE KINASE EXPRESSION.

-! SUBUNIT: EFFICIENT DAM BINDING REQUIRES DIMERIZATION WITH ANOTHER BHILH PROTEIN. HETERODIMER WITH THE ARMY PROTEIN.

-! SUBCELLULAR LOCATION: UNCLEAR (POCENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IN LOWG, FOLLOWED BY HEART, KIDNEY, BRAIN AND LIVER. PREDOMINANTY
EXPRESSED IN ENDOTHELIAL CELLS. ALSO FOUND IN SMOOTH MUSCLE CELLS
OF THE UTERUS, NEURONS, AND BROWN ADIPOSE TISSUE. HIGH EXPRESSION
IN EMBRYONIC CHOROID PLEXUS AND KIDNEY GLOMEROLI.
DEVELOPMENTAL STAGE: IN DAY 11 EMBRYO, EXPRESSION IS ALMOST
EXCLUSIVELY SEEN IN ENDOTHELIAL CELLS OF THE INTERSEGMENTAL BLOOD
VESSELS. SEPARATING THE SOMITES, THE ATRIAL AND VENTRICULAR
CHAMBERS OF THE HEART, AND THE DORSAL AORTA. HIGH EXPRESSION ALSO
COCKURS IN EXTRA-EMBRYONIC MEMBRANES. IN THE DEVELOPING BRAIN OF
DAY 13 EMBRYO, ENDOTHELIAL CELLS OF THE HIGHLY VASCULARIZED
CHOROID PLEXUS CONTAIN HIGH LEVELS OF PERSIL.
  634 TCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCTGCCGGAGCCCTCGC 693
                                       195 ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr 212
                                                                                                                                                                                                                          PASI_MOUSE
P97481; 008787; 055046;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 41, Last annotation update)
15-IUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/6; TISSUE-Hypothalamus, and Skeletal muscle; MEDLINE-97272213; PubMed=9113979; Ema M., Taya S., Yokotani N., Sogawa K., Matsuda Y., Fujil-Kuriyama Y.; "A novel bHLH-PAS factor with close sequence similarity to hypoxia-inducible factor lalpha regulates the VEGF expression and is potentially involved in lung and vascular development."; Proc. Natl. Acad. Sci. U.S.A. 94:4273-4278(1997).
                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97152468; PubMed=9000051;
Jahan H., McKnight S.L., Russell D.W.;
"Endothelial PAS domain protein 1 (EPAS1), a transcription factor
selectively expressed in endothelial cells.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "HRF, a putative basic helix-loop-helix-PAS-domain transcription factor is closely related to hypoxia-inducible factor-1 alpha and developmentally expressed in blood vessels.";
Mech. Dev. 63:51-60(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Brain capillary;
MEDLINE-97321546; PubMed-9178256;
Flamme I., Froehlich T., von Reutern M., Kappel A., Damert A.,
                                                                                        694 TCCGAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCC 741
                                                                                                               213 LysLysProProMetThrCysLeuValLeuIleCysGluProIlePro 228
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
-!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GACGCGCCCGCAGCCGGCGCAGCCAGGAGACGGAGGTGCTGTACCAGCTGGCGCACACT 138
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HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
          TRANSCRIPTION FACTORS. HIGHEST TO HIF-1 ALPHA.
-i- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-i- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
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Mismatches:
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K -> KS (IN REF.
VS -> AA (IN REF.
D -> G (IN REF. 3
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TIGRFAMS; TIGR00229; sensory_box; 2.
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K -> KS
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PAS 2.
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TRANSFAC: T02719;
MGD: MGI:109169; Epas1.
InterPro: IPR001092; HH_basic.
InterPro: IPR001610; PAC.
InterPro: IPR001014; PAS_domain.
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PROSITE; PS50112; PAS; 2.
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SMART; SM00086; PAC; 1.
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Pfam; PF00989; PAS; 2.
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|LeuProLeuProHisSerValSerSerHisLeuAspLysAlaSerIleMetArgLeuAla
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Tian H., McKnight S.L., Russell D.W.;
Endothelial PAS domain protein 1 (EPASI), a transcription factor selectively expressed in endothelial cells.";
Genes Dev. 11:72-82(1997).
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099814: Q99630;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Endothelial PAS domain protein 1 (EPAS-1) (Member of PAS protein
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Catarrhini; Hominidae; Homo.
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MEDLINE-97236817; PubMed-9079689;
                                                      ATCAGCTACCTGCGCATGCACCGCCTC-
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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                                                      ELEMENT (HRE). REGULATES THE VASCULAR ENDOTHELIAL GROWTH FACTOR (VECF) EXPRESSION AND SEEMS TO BE IMPLICATED IN THE DEVELOPMENT OF BLOOD VESSELS AND THE TUBLULAR SYSTEM OF LUNG. MAY ALSO PLAY A ROLE IN THE PORMATION OF THE ENDOTHELIUM THAT GIVES RISE TO THE BLOOD BRAIN BARRIER. POTENT ACTIVATOR OF THE TIE-2 TYROSINE KINASE
                                                                                                                                                                           SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN.
SUBCELLULAR LOCATION: NUCLEAR (POCHOLIAL).
TISSUE SPECIFICITY: EXPRESSED IN MOST TISSUES, WITH HIGHEST LEVELS IN PLACENTA, LUNG AND HEART. SELECTIVELY EXPRESSED IN ENDOTHELIAL
                -!- FUNCTION: TRANSCRIPTION FACTOR INVOLVED IN THE INDUCTION OF OXYGEN REGULATED GENES. SPECIFICALLY RECOGNIZES AN 8 BP HYPOXIA RESPONSE
                                                                                                                                                                                                                                                                                                    -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
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DOMAIN.
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                                                                                                                                                                                                                                                                                                                     TRANSCRIPTION FACTORS. HIGHEST TO HIF-1 ALPHA.
-!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION
-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC)
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Matches:
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PAS 2.
272:8581-8593(1997)
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InterPro; IPR000014; PAS_domain.
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Activator; Anglogenesis; Deve
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PROSITE; PS50888; HLH_2; 1.
PROSITE; PS50112; PAS; 2.
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Pfam; PF00789; PAS; 2.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
TIGRPAMS; TIGR00229; sens
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Nambu J.R., Chen W., Hu S., Crews S.T.;
"The Drosophila melanogaster similar bHLH-PAS gene encodes a protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hexapoda;
                                                                      21 AspalaalaargCysArgArgSerLysGluThrGluValPheTyrGluLeualaHisGlu
                                                                                                                                                                                            247 GGGAGAG------CCACTGGACGCCTGCTACCTGAAGGCCCCTGGAGGGTTTCGTCAT
                                                                                                                                                                                                                                   478 GAACTTCAAGACGCCCTGACCCCCAGG-----CCGAACCTGTCAAAGAAGAAGCTGGAA
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                                                                                                   139 CTGCCCTTTGCGCGCGCGCGTCAGCGCGCACCTGGACAAGGCCTCCATCATGCGCCTCACA
                                                                                                                                                      GGTACTCACCGCCGAGGGAGACATGGCTTACCTGTCGGAAAATGTCAGCAACCTGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  652 TACAAGCCC---CCTGCACAGACTTCCCCTGCCGGGAGCCCTCGCTCCGAGCCTCCCCTG
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Bukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapox
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                    19 ATGCCGTTGGGGCTGCAGCGCGTGAGGTCGAACACCGAGCTGCGGAAGGAGGAAGTCGCGG
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Last annotation update)
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US-09-896-791B-2 (1-1100) x PAS1_HUMAN (1-870)
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SIMA OR CG7951.
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                                                      protein; Transcription regulation;
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T -> V (IN REF. 1).
T -> K (IN REF. 1).
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PROSITE; PS50112; PAS; 2.
Repeat; DNA-binding; Nuclear
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Best Local Similarity:
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247 ----GGGAGACCACTGGACGCCTGCTACCTGAAGGCCCTGGAGGGTTTCGTCATGGTACT 303
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             CAGCAGAGGGCGCACGCTCAACCTCAAAGCGGCCACCTGGAAGGTGCTGCACTGCTCAGG
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yHisLeuValVal-AsnAlaLysGlyGluArgLeuLeuMetAlaIleGlyArgProIleP
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                                              364 TCA-GIGGACCICIGITCCICCICCIGAIACAIAACCCCACICCIGGIACCAAIIICIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                      O.F.
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                                                                                                                                                               TISSUE=Brain;
MEDLINE=97165088; PubMed=9012850;
Zhou Y.-D., Barnard M., Tian H., Li X., Ring H.Z., Francke U.,
Zhou Y.-D., Barnard M., Tian H., Li X., Ring H.Z., Francke U.,
Shelton J., Richardson J., Russell D.W., McKnight S.L.;
"Molecular characterization of two mammalian bHLH-PAS domain proteins selectively expressed in the central nervous system.";
Proc. Natl. Acad. Sci. U.S.A. 94:713-718(1997).
                                                                                                                                                                                                                                                                                                                                                                   pathway.";
J. Biol. Chem. 272:8581-8593(1997).
-!- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN.
                                            protein
                                                                                                                                                                                                                                                                                                                                                                                                                   -i- SUBCELLULAR LOCATION: Nuclear (Potential).
-i- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY
TRANSCRIPTION FACTORS.
-i- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-i- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BY SIMILARITY)
                                                                                                                                                                                                                                                                                    TISSUE-Hepatoma; MEDLINE=97236817; PubMed=9079689; MEDLINE=97236817; PubMed=9079689; Progenesch J.B., Chan W.K., Jackiw V.H., Brown R.C., Gu Y.-Z., Pray-Grant M., Perdew G.H., Bradfield C.A.; "Characterization of a subset of the basic-helix-loop-helix-PAS superfamily that interacts with components of the dioxin signaling
                                                                Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein; Transcription regulation.
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuronal PAS domain protein 1 (Neuronal PASI) (Member of PAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      T -> P (IN REF. 2).
S -> P (IN REF. 2).
V -> A (IN REF. 2).
E1EFB50040A2E7D1 CRC64;
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HELIX-LOOP-HELIX MOTIF
PAS 1.
PAS 2.
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InterPro: IPR001610; PAC.
InterPro: IPR000014, PAS_domain.
Pfam; PF00989; PAS; 1.
SWART; SW000353; HLH; 1.
SWART; SW00086; PAC; 1.
SWART; SW00081; PAS; 2.
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PROSITE; PSS0888; HLH_2; 1.
PROSITE; PSS0112; PAS; 1.
Repeat; DNA-binding; Nuclear
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MIM; 603346; -.
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590 AA;
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                                                                                                                                                                                                      TCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGCGCAGCAGGT---
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 590
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                            Conservative:
Mismatches:
Indels:
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    Length:
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1.21e-16
340.50
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                                         61 CGGAAGGAGAAGTCGCGGGACGCGGCCCGCAGCCGGCGCAGGAGAAGACGGAGGTGCTG 120
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  US-09-896-791B-2 (1-1100) x NPA1_MOUSE (1-594)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                   Zhou Y.-D., Barnard M., Tian H., Li X., Ring H.Z., Francke U., Shelton J., Richardson J., Russell D.W., McKnight S.L.; Molecular characterization of two mammalian bHLH-PAS domain proteins selectively expressed in the central nervous system."; Proc. Natl. Acad. Sci. U.S.A. 94:713-718(1997).

-!- SUBBNAT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -1- SUBCELLULAR LOCATION: Nuclear (Potential).
-1- TISSUE SPECIFICITY: IN BRAIN, EXCLUSIVELY NEURONAL. ALSO FOUND IN SPINAL CORD.
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BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
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-1- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    D6477696DF69A4B3 CRC64
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Conservative:
Mismatches:
Indels:
                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuronal PAS domain protein 1 (Neuronal PAS1)
                                                                             594 AA
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PAS 2.
                                                                               PRT;
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InterPro; IPR001092; HLH_basic.
InterPro; IPR001019; PAC.
InterPro; IPR001014; PAS_domain.
Pfam; PF00989; PAS; 1.
SMART; SM00353; HLH; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00038; HLH_1; 1.
PROSITE; PS00038; HLH_1; 1.
PROSITE; PS50888; HLH_2; 1.
REPEAL; DNA-binding; Nuclear prote DNA_BIND A66558
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                                                                               STANDARD;
                                                                                                                                                                                                                        Mus musculus (Mouse).
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366
212
594 AA;
318 CysGluSer 320
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Best Local Similarity:
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                                                          NPA1_MOUSE
                                                                                                                                                                                                 NPAS1
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
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SRSAGRPSGRSHRQAFSGSSFTPKVQQMEGRTVYARYKLIY
TETTILIELRSRLLDFYRRCWCRGLGRSWEMGRGTAHSCPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTNPY PPOOTSFOMDK LECSQVGNWRTSPPTNAVAPPEQQ
LHSEASDL -> KNQPISPTAPSKWTNWSAARWETGELVPP
QMLWLPRNSSSIQKPAT (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S -> T (IN REF. 3).
P -> R (IN REF. 3).
APRQASRDAARLALARAPPECCAPP -> VLARRPGRARCM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      42 IleIleArgLeuThrThrSerTyrLeuLySMetArgAlaValPheProGluGlyLeuGly
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  184 ATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGCGCAGCAGGT---
                                                                                                                                                                                                                                                                   SWART; SM00091; PAS; 2.
PROSITE; PS00038; HLHL1; 1.
PROSITE; PS50188; HLHL2; 1.
DEVGIOPMENTE; PS50112; PAS; 2.
Developmental protein; Neurogenesis; Nuclear protein; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AGFHGAEHPGVNL (IN REF. 3)
C7904CD24COABBAF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WES (IN REF. 3).
QA -> HG (IN REF. 3).
A -> R (IN REF. 2).
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E -> G (IN REF. 3).
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Conservative:
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                                                                                                                                                                                                                                                                                                                                                                                                                PAS 1.
PAS 2.
                                                                                     EMBL; U40576; AAA91202.1; --
EMBL; D64135; BAA11013.1; --
MGD; MGI: 98307; Sim2.
InterPro; IPR001092; HLH_basic.
InterPro; IPR001610; PAC.
InterPro; IPR001610; PAC.
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                                                       EMBL; U42554; AAB19098.1; -.
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42.35%
30.12%
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Pfam; PF00989; PAS; 2.
SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BIOL. Chem. 272:44:1-4457(1997).

FUNCTION: TRANSCRIPTION FACTOR THAT MAY BE A MASTER GENE OF CNS DEVELOPMENT IN COOPERATION WITH ARNT. IT MAY HAVE PLEIOTROPIC EFFECIENT IN SHE TISSUES EXPRESSED DURING DEVELOPMENT.

SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHIH PROTEIN. HETERODIMER OF SIM2 AND ARNT.

SUBCELLULAR LOCATION: NUCLEAR (PORTILAL).

TISSUE SPECIFICITY: TRANSCRIPTS WERE DETECTED IN HIGH LEVELS IN KIDNEY FOLLOWED BY SKELETAL MUSCLE AND LUNG. LOW LEVELS WERE FOUND IN TESTIS. BRAIN AND HEART.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
                                                                                                                                                                                                                                                                                                                   minima Suruki M., Morita M., Hirose K., Sogawa K., Matsuda Y.,
Gotoh O., Saijoh Y., Fujii H., Hamada H., Fujii-Kuriyama Y.;
"CDNA cloning of a murine homologue of Drosophila single-minded, its
MRNA expression in mouse development, and chromosome localization.";
Biochem. Biophys. Res. Commun. 218:588-594(1996).
                                                                                                                                         TISSUE-Fetal kidney;
MEDLINE-96299751; PubWed-8661115;
MOFIELT P., Dayo M., Reece M., McCormack M.K., Pelletier J.;
"Characterization of msim, a murine homologue of the Drosophila sim transcription factor.";
Genomics 35:144-155(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS. SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-ICR X Swiss Webster; TISSUE-Embryo;
MEDLINE-96299750; PubWed-8661114;
Yamaki A., Noda S., Kudoh J., Shindoh N., Maeda H., Minoshima S.,
Kawasaki K., Shimizu Y., Shimizu N.;
"The mammalian single-minded (SIM) gene: mouse cDNA structure and diencephailc expression indicate a candidate gene for Down
                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Probst M.R., Fan C.M., Tessier-Lavigne M., Hankinson O.; "Two murine homologs of the Drosophila single-minded protein that interact with the mouse aryl hydrocarbon receptor nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-Swiss Webster;
MEDLINE=97020303; PubMed=8812055;
Fan C.M., Kuwana E., Bulfone A., Fletcher C.F., Copeland N.G.,
Jenkins N.A., Crews S., Martinez S., Puelles L., Rubenstein J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression patterns of two murine homologs of Drosophila singlateminded suggest possible roles in embryonic patterning and the pathogenesis of Down syndrome."; Mol. Cell. Neurosci. 7:1-16(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN CNS, DEVELOPING KIDNEY, TONGUE EPITHELIUM AND CARTILAGE PRIMORDIA.
Single-minded homolog 2 (SIM transcription factor) (mSIM)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97172525; PubMed=9020169;
                                                                                                                                                                                                                                                                                                        MEDLINE=96144720; PubMed=8561800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomics 35:136-143(1996).
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                                   musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pessier-Lavigne M.;
                                                                                                                          SEQUENCE FROM N.A.
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                                                                                        NCBI_TaxID=10090;
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-----GCCCAGCTATCCTTAGCCCAGAAACCCACAAATGTCTCCAAAAACCACATAAAG 1014
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                                                                                            LeuArgMetLysCysValLeuAlaLys-----ArgAsnAlaGlyLeuThrCysSerGly 179
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-------GlyGlnValThrThrLysTyrArgLeuLeuSerLysLeuGlyGly 303
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338 LysGluLeuGlnLeuSerLeuAspGlnValSerThrSerIbsSerGlnGluSerTrpArg
                                                                               CACAGTATCTTTGATTTTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACC
                                                                                                                             CCCAGGCCGAACCTGTCAAAGAAGAAGCTG - - - GAAGCCCCAACAGAGCGCCACTTTTCC
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| CysAspThrPheHisLeuArgTyrAlaHisHisLeuLeuValLys------
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                                 TCCTCCTCCTGATACATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGA
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15-JUL-1998 (Rel. 36, Last sequence update)
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                                                                                                                                                                      21
                                                                                                          MEDLINE-97343329; PubMed-9199934; Chrast R., Scott H.S., Chen H., Kudoh J., Rossier C., Minoshima S., Wang Y., Shimizu N., Antonarakis S.E.; "Cloning of two human homologs of the Drosophila single-minded gene SIMI on chromosome 6q and SIM2 on 21q within the Down syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY).
                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 CAGCTGGCGCACACTCTGCCCCTTTGCGCGGGGGTCAGCGCGCACCTGGACAAGGCCTCC
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Conservative:
Mismatches:
 Last annotation update)
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InterPro; IPR001014; PAC.
InterPro; IPR001014; PAS_domain.
Pfam; PF00785; PAS; 2.
SMART; SM00035; HLH, 1.
SMART; SM00085; PAC; 1.
SMART; SM00096; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00091; PAS; 2.
PROSITE; PS50012; PAS; 2.
PROSITE; PS50112; PAS; 2.
Developmental protein; Neurogenesis; Nuclear Transcription regulation; DNA_binding.
Transcription regulation; DNA_binding.
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TRANSFAC; T03729; -.
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312.50
51.80%
36.94%
15.55%
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15-JUN-2002 (Rel. 41, Single-minded homolog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AA;
                                                                                     [1]
SEQUENCE FROM N.A.
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77
218
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DOMAIN
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  SEQUENCE FROM N.A.
MEDLINE=20289799; PubMed=10830953;
Hattori M., Fujlyama A., Taylor T.D., Watanabe H., Yada T.,
Park H.-S., Toyoda A., Ishii K., Totoki Y., Choi D.-K., Soeda E.,
Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Polley A.,
Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D.,
                                                                                                                                                                                                                                                             618
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                                                                                                                                    82 SerHisLeu-LeuGlnThrLeuAspGlyPheIlePheValValAlaProAspGlyLysIl 101
                                                                                                                                                                                                                            81
                                            61
22 GluLeuAlaLysLeuLeuProLeuAlaSerAlaIleThrSerGlnValAspLysAlaSer 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97343329; PubMed=9199934; Chrast R., Scott H.S., Chen H., Kudoh J., Rossier C., Minoshima S., Wang Y., Shimizu N., Antonarakis S.B.; "Cloning of two human homologs of the Drosophila single-minded gene SIM1 on chromosome 6q and SIM2 on 21q within the Down syndrome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14)
SEQUENCE FROM N.A.
Shibuya K., Kudoh J., Minoshima S., Kawasaki K., Nakatoh E.,
Shibuya K., Asakawa S., Shimizu N.;
"Genomic sequencing of 1.2-Mb region on human chromosome 21q22.2.";
Shimitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                262 CGCCTGCTACCTGAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACAT
                                                                                                                                                          442 AGTATCTTTGATTTTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCC
                                                                                       62 GluAlaTrpGlyHisSerSerArgThrSerProLeuAspAsnValGlyArgGluLeuGly
                                                                                                                                                                                                     382 TCCTCCCTGAIACATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGACAC
                                                                                                                                                                                                                                                                                             --- AGGCCGAACCTGTCAAAGAAGAAGCTGGAAGCCCCCAACAGAGCGCCACTTTTCCCTG
                                                                                                                                                                                                                                                                                                                  143 HisGlnProTyrHisSerHisPheValGlnGluTyrGluIleGluArgSerPheLeu
                                                                                                                                                                                                                                                                                                                                         CGAATGAAGAGCACGCTCACCAGCAGAGGGCGCACGCTCAACCTCAAAGCGGCCACCTGG
                                                                                                                                                                                                                                                                                                                                                              163 ArgMetLysCysValLeuAlaLys-----ArgAsnAlaGlyLeuThrCysGlyGlyTyr
                                                                                                                                                                                                                                                                                                                                                                                    619 AAGGTGCTGCACTCCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCT
                      184 ATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGCGCAGCAGGT-----
                                                                   -----GGAAAAGGGGGAGAGCCACTGGA
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                       SIM2_HUWAN STANDARD; PRT; 667 AA. 014190; Q15470; Q15471; Q15472; Q15473; Q16532; Q1-NOV-1997 (Rel. 35, Created) 15-JUL-1998 (Rel. 36, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) single-minded homolog 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosomal region.";
Genome Res. 7:615-624(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (Human)
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -:- FUNCTION: TRANSCENDION FACTOR THAT MAY BE A MASTER GENE OF CNS
-:- FUNCTION: TRANSCENPTION WITH ARNT. IT MAY HAVE PLEIOTROPIC
EFECTS IN THE TISSUES EXPRESSED DURING DEVELOPMENT.
-:- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
BHLH PROTEIN. HETERODIMER OF SIM2 AND ARNT.
-:- SUBCELLULAR LOCATION: Nuclear (Potential).
-:- ALTERNATIVE PRODUCTS: 2 ISOFORMS; SIM2 (SHOWN HERE) AND SIM2S; ARE
PRODUCED BY ALTERNATIVE SPLICING.
-:- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W., Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shinton A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis S.E., Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P., Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloecker H., Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Dagand E., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis F., Lehrach H., Reinhardt R., Yaspo M.-L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Dahmane N., Charron G., Lopes C., Yaspo M.-L., Maunoury C., Decorte L., Sinet P. M., Bloch B., Delabar J.M.; M.; M. Bown syndrome-critical region contains a gene homologous to Drosophila sim expressed during rat and human central nervous system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-95375794; PubMed=7647800;
Chen H., Chrast R., Rossier C., Gos A., Antonarakis S.E., Kudoh J.,
Yamaki A., Shindoh N., Maeda H., Minoshima S., Shimizu N.;
"Single-minded and Down syndrome?";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TRANSCRIPTION FACTORS.
-!- SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-!- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yamaki A., Noda S., Kudoh J., Shindoh N., Maeda H., Minoshima Rawasaki K., Shimizu Y., Shimizu Y., "The mammalian single-minded (SIM) gene: mouse cDNA structure diencephalic expression indicate a candidate gene for Down
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Osoegawa K., Okano S., Soeda E.;
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 1-58; 87-152; 183-247 AND 249-283 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 92:9191-9195(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 87-116 FROM N.A.
MEDLINE-96016135; PubMed-7568099;
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EMBL, U80457; AAB62397.1; -.
EMBL, AB003185; BAA21489.1; -.
EMBL, AB003185; BAA21490.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1-247 FROM N.A.
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970 TCCTTAGCCCAGAAACCCACAAATGTCTCCAAAACCACCATAAAGACCTCTCCTTGTTAG 1029
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     123 SerIleTyrGluTyrIleHisProSerAspHisAspGluMetThrAlaValLeuThrAla 142
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233 MetPheArgAlaSerLeuAspLeuLysLeuIlePheLeuAspSerArgValThrGluVal
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293 LysTyrTyrArgLeuLeuSerLysArgGlyGlyTrpValTrpValGlnSerTyrAlaThr
                                                              502 AGGCCGAACCTGTCAAAGAAGAAGCTG---GAAGCCCCCAACAGAGCGCCCACTTTTCCCTG
                                                                                              CGAATGAAGAGCACGCTCACCAGCAGAGGCGCACGCTCAACCTCAAAGCGGCCACCTGG
                                                                                                                                                                                                                                                                                   AAGGTGCTGCACTGCTCAGGACATATGAGGCCGTACAAGCCCCCTGCACAGACTTCCCCT
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
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MEDLINE=97020303; PubMed=8812055;
Fan C.-M., Kuwana E., Bulfone A., Fletcher C.F., Copeland N.G.,
Jenkins N.A., Crews S., Martinez S., Puelles L., Rubenstein J.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -------CCACAG------GAGAAGACTCCCATC-----
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R SMART; SM00091; PAS; 2.

R PROSITE; PS50189; HLH_1; 1.

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GASVIITHGR -> HEFSSKEMLPAKFGQPQGSPCBVARF
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1 Biol. Chem. 272:4457(1997).

2 Biol. Chem. 272:4457(1997).

3 Biol. Chem. 272:451-457(1997).

3 Biol. Chem. 272:451-457(1997).

3 BIUR RENORING PRENORE THAT MAY HAVE PLEIOTROPIC FEFECTS

3 BULH PROTEIN HETERODINER OF SIMI AND ARNT.

4 SUBGELLULAR LOCATION: NUCLEAR (POLATIAL).

5 SUBGELLULAR LOCATION: NUCLEAR (POLATIAL).

5 SUBGELLULAR LOCATION: NUCLEAR (POLATIAL).

6 SUBGELLULAR LOCATION: NUCLEAR (POLATIAL).

7 TISSUE SPECIFICITY: DETECTED IN LUNG, SKELETAL MUSCLE AND KIDNEY.

8 SOMITES, MESONERMAL AND ENDOREMAL TISSUES, INCLUDING DEVELOPING

8 SOMITES, MESONERMAL AND ENDOREMAL TISSUES, INCLUDING DEVELOPING

9 SOMITES, MESONERMAL AND ENDOREMAL TISSUES.

1 SAMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.

1 SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
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Two new members of the murine Sim gene family are transcriptional repressors and show different expression patterns during mouse
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                                                                                                                     Fan C.-M., Kuwana E., Bulfone A., Fletcher C.F., Copeland N.G., Jenkins N.A., Crews S., Martinez S., Puelles L., Rubenstein J.L., Tessier-Lavigne M.;
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Wang Y., Shimizu N., Antonarakis S.E.;
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EMBL, AB013494; BAA28270.1; --
EMBL, AB013485; BAA28270.1; JOINED.
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EMBL, AB013486; BAA28270.1; JOINED.
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22 GluLeuAlaLysLeuLeuProLeuProSerAlaIleThrSerGlnLeuAspLysAlaSer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ------GGAAAAAGGGGGAGAGCCACTGGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---AGGCCGAACCTGTCAAAGAAGAAGCTGGAAGCCCCAACAGAGCGCCCACTTTCCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  162 CGCCTGCTACCTGAAGGCCCTGGAGGTTTCGTCATGGTACTCACCGCCGAGGGAACAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R InterPro; IPR001092; HLH_basic.
R InterPro; IPR001092; HLH_basic.
R InterPro; IPR00101067; Nuc_translocat.
R InterPro; IPR00101067; Nuc_translocat.
R InterPro; IPR000104; PAC.
R InterPro; IPR000014; PAS.
R PEAM; PF00785; PAC; 1.
R SMART; SM00085; PAC; 1.
R SMART; SM00081; PAC; 1.
R SMART; SM00081; PAC; 1.
R PROSITE; PS00038; HLH_1: 1.
R PROSITE; PS00038; HLH_2: 1.
R PROSITE; PS00112; PAS; 2.
R PROSITE; PS00112; PAS; 2.
R PROSITE; PS00112; PAS; 2.
R PROSITE; PS00112; PAS; 3.
R PROSITE; PS00112; PAS; 4.
R PROSITE; PS00112; PAS; 5.
R PROSITE; PS00112; PAS; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CRC64;
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82
32
70
38
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MISSING (IN REF. 1).
P -> R (IN REF. 1).
P -> R (IN REF. 1).
D -> S (IN REF. 1).
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Matches:
Conservative:
Mismatches:
Indels:
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DNA_BIND 1 13 RACTO DOWN
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PAS 2.
                           BAA28270.1; JOINED.
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51,35%
36,94%
15,45%
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Best Local Similarity:
EMBL; AB013489;
                              AB013490;
                                                             MGD; MGI:98306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
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DOMAIN
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CONFLICT
CONFLICT
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Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
R.A. Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
R.A. Adams M.D., Celniker S.E., Holf P.W., Hoskins R.A., Galle R.E.,
R.A. George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
R. Sutton G.G., Wortman J.R., Yandaell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfelffer B.D.,
R.A. Brandon R.C., Bayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
R. Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
R. Besson K.Y., Bencos P.V., Berman B.P., Bhandari D., Botther P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
R.A. Borkova D., Delcher A., Deng Z., Mays A.D., Dew I. J. Dietz S.M.,
A de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I. J., Dietz S.M.,
R.A. Dorbon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
R.A. Dorbon K., Doup L.E., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
R.A. Fosler C., Gabriellan A.E., Garraz C., Ferriers S., Felischmann W.,
R.A. Fosler C., Gabriellan A.E., Garraz C., Kenrisc M., Harris M.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
R.A. Lasko P., Lei Y., Levitsky A.A., Li J., Hernandez J.R., Ruth D., Lai Z.,
R.A. Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
A Lasko P., Lei Y., Wobarry C., Morris J., Mosherson D.,
R.A. Mattel B., McIntosh T.C., McLeod M.P., Morris J., Mosherson D.,
R.A. Hastingn G., Milshina N.V., Mobarry C., Morris J., Mosherson D.,
R. Alasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Evese M.G.,
R. Ralman B., Rolling R.A., Nivoh B., Pollar F., Pollar F., Rese M.G.,
R. Palazzolo W., Piltiman G.S., Pollar G., Pollar F., Rese M.G.,
R. Palazzolo W., Piltiman G.S., Pollar F., Pollar F., Rese M.G.,
                               618
                                                           180
                                                                                        678
                                                                                                      143 HisGlnProTyrHisSerHisPheValGlnGluTyrGluIleGluArqSerPhePheLeu 162
                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Bukaryota; Metazoa, Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoplera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isaac D.D., Andrew D.J.; "Tubulogenesis in Drosophila: a requirement for the trachealess gene
                             559 CGAATGAAGAGCACGCTCACCAGCAGAGGGCGCACGCTCAACCTCAAAGCGGCCACCTGG
                                                         163 ArgMetLysCysValLeuAlaLys-----ArgAsnAlaGlyLeuThrCysGlyGlyTyr
                                                                                     619 AAGGTGCTGCACTCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
                                                                                                                                                                                                                                                                                                                                                                                                                   Wilk R., Weizman I., Shilo B. Z.;
"Trachealess encodes a bHLM-PAS protein that is an inducer of tracheal cell fates in Drosophila.";
Genes Dev. 10:93-102(1996).
                                                                                                                                                                           STRAIN-Berkeley;
MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Embryo;
MEDLINE=96136712; PubMed=8557198;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96136713; PubMed-8557189;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genes Dev. 10:103-117(1996).
                                                                                                                                                                                                                                                      Trachealess protein.
                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Embryo;
                                                                                                                                                                                                                                                                     TRH OR CG6883
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DECELUIAR LOCATION: NUCLEAR.

- I- SUBCELUILAR LOCATION: NUCLEAR.

- I- ALTERNATIVE PRODUCTS: AT LEAST 3 ISOFORMS; 1 (SHOWN HERE), 2 AND 3; ARE PRODUCED BY ALTERNATIVE SPLICING.

- I- TISSUE SPECIFICITY: TRACHEA, SALIVARY GLAND DUCTS, POSTERIOR SPIRACLES (FILZKOEBER PRINGARIA) AND A SUBSET OF CELLS IN THE CONS.

- I- DEVELOPMENTAL STAGE: DURING EMBRYOGENESIS, FIRST DETECTED IN THE CONS.

- I- DEVELOPMENTAL DEVELOPMENT: IN THE DEVELOPING SALIVARY GLAND, EXPRESSION IS OBSERVED IN THE ENTIRE GLAND AT STAGE 9 AND BY STAGE 12, EXPRESSION IS CONFINED TO THE SALIVARY DUCTS.

- IS STALLARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS.

- I- SIMILARITY: CONTAINS 2 PAS (PER ARNT-SIM) DIMERIZATION DOMAINS.

- I- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

- I- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

- I- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

- I- SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.

- II POSITIONS 22 TO 34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Wang Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao O.A. Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng T., Mark S., Zhu X., Zhu S., Zhu X., Smith H.O., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; The genome sequence of Drosophila melanogaster."
                                                                                                                                                                                                                                                                                                           FUNCTION: TRANSCRIPTION FACTOR, MASTER REGULATOR OF TRACHEAL CELL FATES IN THE EMBRYC, NECESARY FOR THE DEVELOPMENT OF THE SALLYARY GLAND DUCT AND THE POSTERIOR SPIRACLES. IT MAY INDUCE A GENERAL FATE OF BRANCHED TUBULAR STRUCTURES OF EPITHELIAL ORIGIN. TGO/TRH HETERODIMERS ARE INVOLVED IN THE CONTROL OF BREATHLESS EXPRESSION.

- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHLH PROTEIN. HETERODIMER WITH TGO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
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HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro: IPR001092; HLH_basic.
InterPro: IPR001092; HLH_basic.
InterPro: IPR001014; PAC.
InterPro: IPR000014; PAC.
InterPro: IPR000014; PAC.
SMART: SM00086; PAS; 2.
SMART: SM00086; PAC; 1.
SMART: SM00091; PAC; 1.
SMART: SM00091; PAC; 1.
PROSITE; PS500038; HLH_1; 1.
PROSITE; PS50018; PAS; 2.
Developmental protein; Nuclear protein; Transcription regulation; Repeat; DNA-binding; Alternative splicing.
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POLY SER.
POLY GLY.
POLY GLY.
MISSING (IN ISOFORM 2
MISSING (IN ISOFORM 3
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-> GG (IN REF. 2).
-> T (IN REF. 1).
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EMBL; U42699; AAA96754.1; ALT_FRAME.
EMBL; AE003468; AAF47386.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PAS 1.
PAS 2.
PAC.
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                                                                                                                                                                            SerGlyTyrArgAlaSerAspAlaThrSerAsnCysAsnAsnGlyAsnAsnAlaSerAsn 343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          344 AsnAlaLysAsnValLysAsnProGlySerAsnTyrSerValValLeuLeuLeuCysLys 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                  :::||| :::|||
145 GlyAspProProTrpThrArgGluAlaSerSerSerSerLysLeuLysSerAlaAlaIle
                                                                                                                                                                                                                                                                                                                                                                                                    CCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATGGCTTACCTGTCGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 AspvalAlaAlaSerMetThrGlnAlaSerThrSerGlyTyrLysGlyTyrAspArgSer
                                                                                                                                                                                                                              220 ------CGCCTCTGCGCAGCAGGTGGA
                                                                                                                                                                                                                                                                                                                                                                                    --- GGACGCCTGCTACCTGAAGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    340 IGTCAGCAAGCACCTGGGCCTCAGTCAGTGGACCTCTGTTCCTCCTCCTCCTGATACATAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             226 HisGlnAlaAspHisSerGluIleAlaAspGlnLeuGlyLeuSerLeuThrSerGlyGly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 246 GlyGlyGlyGlyGlySerSerSerSerGlyGlyGlyGlyGlyGlyAlaGlyGlyGlyMet
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -------ACCCCAGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   266 AlaSerProThrSerGlyAlaSerAspAspGlySerGlyThrHisGlyThrAsnAsnPro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      306 PheCysValArgMetLysSerThrLeuThrLysArgGly-----CysHisPheLysSer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -- CACTGCTCAGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                550 TTTTCCCTGCGAATGAAGAGCACGCTCACCAGGAGGGCGCACGCTCAACCTCAAAGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       460 CATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTG--------
-> P (IN REF. 1).
-> V (IN REF. 1).
8F9CF758F1370541 CRC64;
                                                            958
96
46
72
122
8
                                                                                                                                                                                                                                                                               175 AAGGCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCAC--
                                                                                    Conservative:
Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204 rValSerIleTyrLeuGlyLeuSerGln------
                                                            Length:
Matches:
                                                                                                                                                    US-09-896-791B-2 (1-1100) x TRH_DROME (1-958)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CATATGAGGGCCTACAAGCCCCCTGCA-----
708 A
829 A
102241 MW;
 A A
                                                           5.68e-14
302.50
42.26%
28.57%
15.05%
                                                                                                                                                                                                                                                                                                                                                                                  241 AAAAGGGGAGAGCCACT----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCCACCTGGAAGGTGCTG-
708
829
958 AA;
                                                                                                  Best Local Similarity:
Query Match:
                                                                                      Percent Similarity:
                                                  Alignment Scores:
CONFLICT
                         SEQUENCE
                                                               Pred. No.:
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RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holf P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Backer E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Apdayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Brill J.F., Apdayani A., An H.-J., Andrews Pfannkoch C., Baldwin D.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Hostin D., Haurey D., Heiman T.J., Harnandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwan C.,
RA Liu X., Mattei B., McIntosh T.C., Morris J., Moshrefi A.,
RA Liu X., Mattei B., McIntosh T.C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein
---CAGACTTCCCCTGCCGGGAGCCCTCGCTCCGAGCCTCCCCTGCATGCCTG 717
                       Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDILINE-9904545; PubMed-9840810;
MEDILINE-9904545; Crews S.;
"Specification of the Drosophila CNS midline cell lineage: direct control of the Drosophila CNS midline phy dorsal/ventral patterning control of single-minded transcription by dorsal/ventral patterning cenes."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nuclear protein with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 1-18 FROM N.A., AND SIMILARITY TO HLH PROTEINS. MEDLINE=92103681; PubMed=1760843; MEDLINE=92103681; PubMed=1760843; Nambu J.R., Lewis J.O., Wharton K.A. Jr., Crews S.T.; "The Drosophila single-minded gene encodes a helix-loop-helix pract acts as a master regulator of CNS midline development."; Cell 67:1157-1167(1991).
                                                                                     GTGCTTATCTGTGAAGCCATCCCCCAGCTCCCCTTCCACGAT 759
                                                                                                                              384 ValAlaLeuAlaIleAlaLeuProProProSerValHisGlu 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Crews S.T., Thomas J.B., Goodman C.S.;
"The Drosophila single-minded gene encodes a nu
sequence similarity to the per gene product.";
Cell 52:143-151(1988).
                                                                                                                                                                                                                    SIM_DROME STANDARD; PRT; 673 AA. P05709; 096521; Q9VF23; 01-NOV-1988 (Rel. 09, Created) 01-MAY-1992 (Rel. 22, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Single-minded protein.
                                                                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=Berkeley;
MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 19-673 FROM N.A.
MEDLINE=88151023; PubMed=3345560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gene Expr. 7:171-189(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            SIM OR CG7771
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SIM_DROME
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299
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
Relson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Relson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
Relson D.R., Parliann G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Reinert K., Semington K., Stander R., Shen H.,
Reper E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
Rape E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
Rape S.Y., Wassarman D.A., Welley K.C., Wu D., Yang S., Yao Q.A.,
Rape J.Y., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Reiner R.H., Zhong W., Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@illower.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BHLH PROTEIN.

BUCELLULAR LOCATION: Nuclear (Potential).

SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
TRANSCRIPTION FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS. SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN. CAUTION: Ref.4 sequence differs from that shown due to erroneous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BASIC DOMAIN.
HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TitleTrip i FR000110 FAC.

Refam; PF00785; PAC; 1.

Refam; PR00815; PAC; 1.

Refam; PR00178; PAC; 1.

Reformer: PS50888; HLH_2; 1.

Reformer: PS50888; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEATS OF A-A-Q.
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MISSING (IN REF. 4).
2F9F0ABBA2BCOFBE CRC64;
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POLY-ASN.
POLY-HIS.
POLY-GLN.
POLY-SER.
POLY-SER.
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PAS 2.
14 X 3 AA
POLY-VAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AF071934; AAC64519.1; ALT_SEQ
AE003698; AAF54902.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001092; HLH_basic.
InterPro; IPR001610; PAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gene model prediction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIR; A29945; A29945.
TRANSFAC; T00750; -.
FlyBase; FBgn0004666; sim.
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401 4
673 AA;
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546
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                                                                                                                                                                                                                                                                       184 ATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGCGCAGCAGGT---- 237
                                                                                                                                                                                                                                                                                                                                   -----GGAAAAGGGGGAGAGCCACTGGACGC 264
                                                                                                                                                                                                                                                                                                                                                                                                               |||||||:::::||||||| ||||||:::||||::|
123 IlePheGluTyrIleHisAsnTyrAspGlnAspGluMetAsnAlaIleLeuSerLeuHis 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProHisIleAsnGlnHisProLeuAlaGlnThrHisThrProIleGlySerProAsnGly 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 547 CACTITICCCTGCGAATGAAGAGCACGCTCACCAGCAGAGGGCGCACGCTCAACCTCAAA 606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       667 CAGACTICCCCTGCCGGGAGCCCTCGCTCCGAGCCTCCCTGCAATGCCTGGTGCTTAIC 726
                                                                                                                                                 64 AAGGAGAAGTCGCGGGACGCGCCCCCGCAGCCGGCCAGCAGGAGGTGCTGTAC 123
                                                                                                                                                                                                              124 CAGCTGGCGCACACTCTGCCCTTTGCGCGCGCGCTCAGCGCGCACCTGGACAAGGCCTCC 183
                                                                                                                                                                                                                                                                                                                                                                                               265 CTGCTACCTGAAGGCCCTGGAGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATGGC 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16 -----Val--GluLeuThrGlyAsnSer 122
                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                 22 GluLeuAlaLysLeuLeuProLeuProAlaAlaIleThrSerGlnLeuAspLysAlaSer 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ::: |||:::
163 ValGlnHisProSerAlaTyrAspHisAspArgGlySerHisThrIleGluIleGluLys
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62 GluAlaTrpGlySerSerProAlaMetGlnArgGlyAlaThrIleLysGluLeuGlySer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      101 tTyrIleSerGluThrAlaSerValHisLeuGlyLeuSerGln-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATCTTTGATTTTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             607 GCGGCCACCTGGAAGGTGCTGCACTGCTCAGGACATATGAGGGCCTACAAGCCCCCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    221 ArgGlyAspGlyGlnGlySer------LeuIleGlnAsnLeuGlyLeuVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCCCTGATACATAACCCCCACTCCTGGTACCAATTTCTCTCTGGGGGCTCATTGGACACAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    727 TGT-----GAAGCCATCCCCAGCTCCCCTTCCAC
           673
86
46
73
74
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Mismatches:
            Length:
Matches:
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(Rel. 37, Last sequence update)
                                                                       Indels:
                                                                                                                   US-09-896-791B-2 (1-1100) x SIM_DROME (1-673)
                                                                                     Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGAACCTGTCAAAGAAGAAGCTG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ---GAAGCCCCAACA------
         4.61e-13
289.50
47.31%
30.82%
14.40%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                   238 -----
                                         Percent Similarity:
Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARN2_MOUSE
Q61324;
15-DEC-1998 (
15-DEC-1998 (
Alignment Scores:
                                                                        Query Match:
               NO.
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::: :::|||:::|||::: 81 GlnTyrIleThrGluLeuSerAspMetValProThrCysSerAlaLeuAlaArgLysPro 100

GACAAGGCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGCGCA

172

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101 AspLysLeuThrIleLeuArgMetAlaValSerHisMetLysSerMetArg-----

232 GCAGGTGGAAAAAGGGGGAGAGCCACTGGACGCCTGCTAC-----

112

δ

q

ACCGAGCTGCGGAAGGAGAAGTCGCGGGACGCGGCCCCCAGCCGGCGCAGCCAGGAGACG 111

52

g

61 SerLysPheSerArgGluAsnHisSerGluIleGluArgArgArgArgAsnLysMetThr

-----CTGAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGC

310 CGAG---GGAGACATGGCTTACCTGTCGGAAAATGTCAGCAAGCACCTGGG----CCTCA

118 -----GlyThrGlyAsnLysSerThr-AspGlyAlaTyrLysProSerPheLeuThrGl 135

362

482

TCAAGACGCCCTG---ACCCCCAGGCCGAACCTGTCAAAGAAGAAGCTGGAAGCCCCCAAC 539 195 uArgGluGlnLeuCysThrSerGluAsnSerIleThrGlyArgIleLeuAspLeuLysTh 215

483

ò g ŏ g á g δ qq Ω

g

-----GAGCG 545

567

611

215 rGlyThrValLysLysGluGlyGlnGlnSerSerMetArgMetCysMetGlySerArgAr 235

540 A-----

CCACTTTCCCTGCGAATGAAG-----

546

235 gSerPheIleCysArgMetArgCysGlyAsnAlaProLeuAspHisLeuProLeuAsnAr 255

612

g

ò q 706 AA.

ARN2_HUMAN

----AGCACGCTCACCAGCAGAGGCCCACG-------CTCAACCTCAAAGCGGC

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                                                                                                                                                                                                                                                                                                                            -!-SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BHIH PROTEIN. HETERODIMER WITH THE ARYL HYDROCARBON RECEPTOR (AHR) OR THE SIMI PROTEIN.
-!-SUBCELLULAR LOCATION: Nuclear (Potential).
-!-TISSUE SPECIFICITY: RESTRICTED TO ADULT BRAIN AND KIDNEY.
-!-SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS, HIGHEST TO THE ARNT PROTEINS.
-!-SIMILARITY: CONTAINS 2 PAS (PER-ARNT-SIM) DIMERIZATION DOMAINS.
-!-SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                                                                                                                                                                                                                   -!- FUNCTION: SPECIFICALLY RECOGNIZES THE XENOBIOTIC RESPONSE ELEMENT
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                                                                                                                                   SEQUENCE FROM N.A.
STRAIN=C57BL/65; TISSUE=Embryo;
STRAIN=C9239527; PubMed=6657146;
Hirose K., Morita M., Ema M., Mimura J., Hamada H., Fujii H.,
Saijo Y., Gotoh O., Sogawa K., Fujii-Kuriyama Y.;
"cDMA cloning and tissue specific expression of a novel basic helix-loop-helix-YpAS factor (Arnt2) with close sequence similarity to the aryl hydrocarbon receptor nuclear translocator (Arnt).";
Mol. Cell. Biol. 16:1706-1713(1996).
                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
16-OCT-2001 (Rel. 40, Last annotation update)
Aryl hydrocarbon receptor nuclear translocator 2 (ARNT protein 2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Repeat
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HELIX-LOOP-HELIX MOTIF (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FACD26EEBB7F18DE CRC64;
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Interpro; PR001092; HLL_basic.
Interpro; PR001067; Nuc_translocat.
Interpro; IPR001610; PAC.
Interpro; IPR001610; PAS_domain.
Pfam; PP00010; HLH; 1.
Pfam; PP009099; PAS; 2.
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SMART; SMO0353; HLH; 1.
SMART; SMO0066; PAC; 1.
SMART; SMO0091; PAS; 2.
TIGREAMS; TIGRO0229; SENSORY_DOX; 1.
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PAS 2.
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445 PC
555 PC
77884 MW;
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22.508
8.23$
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DNA_BIND 64 7
                                                 Mus musculus (Mouse)
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                                                                                                      NCBI_TaxID=10090;
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[1]
SEQUENCE FROM N.A.
Barrow L.L., Wines M.E., Romitti P.A., Holdener B.C., Murray J.C.;
                                                                                                                                                          16-0CT-2001 (Rel. 40, Last sequence update)
Aryl hydrocarbon receptor nuclear translocator 2 (ARNT protein 2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
ARN2_HUMAN STANDARD; E 09HBZ; 015024; 116-02T-2001 (Rel. 40, Created) 16-0CT-2001 (Rel. 40, Last sequin C-0CT-2001 (Rel. 40, Last annotation of the core of the co
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712 63 57 80 81

Conservative: Mismatches: Length: Matches:

Best Local Similarity:

Query Match:

Percent Similarity:

Indels:

Gaps:

US-09-896-791B-2 (1-1100) x ARN2_MOUSE (1-712)

us-09-896-791b-2.rsp

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                                                                                                                                                                                                                            (XRE).
SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER BLLH PROTEIN. HETERODIMER WITH THE ARYL HYDROCARBON RECEPTOR (AHR) OR THE SIMI PROTEIN (BY SIMILATLY).
SUBCELLULAR LOCATION: Nuclear (Potential).
SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF TRANSCRIPTION FACTORS. HIGHEST TO THE ARNT PROTEINS.
SIMILARITY: CONTAINS 2 PAS (PER ARNT SIM) DIMERIZATION DOMAINS.
SIMILARITY: CONTAINS 1 PAS-ASSOCIATED C-TERMINAL (PAC) DOMAIN.
                                                                                                           Nagase T., Ishikawa K.I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro."; DNA Res. 4:141-150(1997).
"Aryl-hydrocarbon receptor nuclear translocator 2 (ARNT2): structure, gene mapping, and candidate evaluation for human orofacial clefts."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
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HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
PAS 1.
PAS 2.
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InterPro; IPR001067; Nuc_translocat.
InterPro; IPR0010610; PAC.
InterPro; IPR000141; PAS_domain.
Pfam: PF008091; HIH; 1.
Pfam: PF008095; NASTRSLOCATR.
SMART; SM00853; HIH; 1.
SMART; SM008091; PAS; 2.
TIGRFAMS; TIGR00229; sensory_box; 1.
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EMBL, AF185593, AAG15310.1; --
EMBL, AF185594, AAG15310.1; JOINED.
EMBL, AF185595, AAG15310.1; JOINED.
EMBL, AF185595, AAG15310.1; JOINED.
EMBL, AF185599, AAG15310.1; JOINED.
EMBL, AF185599, AAG15310.1; JOINED.
EMBL, AF185600, AAG15310.1; JOINED.
EMBL, AF185601, AAG15310.1; JOINED.
EMBL, AF185602, AAG15310.1; JOINED.
EMBL, AF185603, AAG15310.1; JOINED.
EMBL, AF185604, AAG15310.1; JOINED.
EMBL, AF185605, AAG15310.1; JOINED.
EMBL, AF185605, AAG15310.1; JOINED.
EMBL, AF185605, AAG15310.1; JOINED.
EMBL, AF185605, AAG15310.1; JOINED.
EMBL, AF185606, AAG15310.1; JOINED.
EMBL, AF185608, AAG15310.1; JOINED.
EMBL, AF185609, AAG15310.1; JOINED.
EMBL, AF185609, AAG15310.1; JOINED.
EMBL, AF185609, AAG15310.1; JOINED.
                                                                                                 MEDLINE-97349984; PubMed-9205841;
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PROSITE; PS50038; HiH_2; 1.
PROSITE; PS50112; PAS; 2.
DNA-binding; Nuclear protein; T; DNA_BIND 53 65 BAK
DOMAIN 66 106 HEI
DOMAIN 312 382 PAK
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                                                                SEQUENCE FROM N.A.
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244 gIleThrThrMetArgLysArgPheArgAsnGlyLeuGlyProValLysGluGlyGluAl 264
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                                                                                                                                                                                                                                                                                                                                                                           184 uArgGluGlnLeuCysThrSerGluAsnSerMetThrGlyArgIleLeuAspLeuLysTh
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       272 -------CTGAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGC
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              POLY-ARG.
POLY-GLN.
POLY-SER.
POLY-SER.
G -> K (IN REF. 2).
G -> S (IN REF. 2).
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63
57
80
81
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Matches:
Conservative:
Mismatches:
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CONFLICT
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09wru9 rattus norv
035800 rattus norv
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09w7c6 gallus gall
09ptb3 coturnix co
09xr4 bos taurus
09jh729 homo sapien
08ggm4 fundulus he
                                                09jhs2 rattus norv
09y2n7 homo sapien
09hai2 homo sapien
09bam5 homo sapien
09cya8 mus musculu
08r385 mus musculu
                                                                                                                                                                                                                                                                                                                                                                                                                     Q9qz94 cavia porce
Q963j8 caenorhabdi
Q45486 caenorhabdi
Q9tvm0 caenorhabdi
                                                                                                               O9xta5 bos taurus
O9yib9 gallus gall
Q96pt9 homo sapien
O9upbl homo sapien
                                                                                                                                                                                                                                                                                                                1 mus musculu
homo sapien
homo sapien
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O98sw2 oncorhynchu
O95262 homo sapien
O9uph7 homo sapien
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O35391 mus musculu
O9h323 homo sapien
                                                                                                                                                                                                                                                                      Q918a9 xenopus lae
Q8r4d6 mus musculu
Q9by83 homo sapien
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015984 bombyx mori
09n110 ovis aries
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070284 mus musculu
  musculu
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                     homo sapien
homo sapien
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Q8sx13 drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Makino Y., Cao R., Svensson K., Bertilsson G., Asman M., Tanaka H., Cao Y., Berkenstam A., Poellinger L.;
"Inhibitory PAS domain protein is a negative regulator of hypoxia-
 Q9qx54 mus
Q9z2i5 mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse),
Sukaryota, Metazoa, Chordata, Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_raxID=10090;
                                                                                                                                                                                                                                                                                                                                                                             9npp60
                     Q8wxa1 |
Q96k34 |
                                                              09y2n7 |
09hai2 |
                                                                                 Q9ham5
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1-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Inhibitory PAS domain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALIGNMENTS
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Q9WTU9
Q35800
Q9JHS1
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Q98SJ5
O15984
 Q9QX54
Q9Z2I5
Q8WXA1
Q96K34
                                        Q8TAP5
Q9JHS2
Q9Y2N7
                                                                      094AI2
094AM5
09CYA8
08R385
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Q9PTB3
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Q8QGM4
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095262
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Q8R4D6
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035391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inducible gene expression.";
Nature 414:550-554(2001).
EMBL; AF416641; AAL39015.1; -.
InterPro: IPR001092; HLH_basic.
SMART; SM00353; HLH; 1.
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STRAIN-C57BL/6J;
Pubmed-11734856;
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309.5
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-MODEL-framet-n2P, model -DEV=Xlp
-MODEL-framet-n2P, model -DEV=Xlp
-MODEL-framet-n2P, model -DEV=Xlp
-MODEL-framet-n2P, model -DEV=Xlp
-DE-SPTREMBL_21 -QFWT-fastan -SUFFIX=rspt -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS-BLIS -START=1 -END=-1 -MATRIX-blosum62 -TRANS-human40 cdi -LIST=45
-DOCALIGN=200 -THR_SCORE-pct -THR_MX=100 -THR_MIN-0 -ALIGN=15 -MODE=LOCAL
-OUTFNT--ptc -NORM-ext -HEAPSIZE=500 -MINEN-0 -MAXLEN=2000000000
-USER-US09896791_eCGN_1_1_66_erunat_02122002_152658_5586 -NCPU=6 -ICPU=3
-NO_XLDXY -NO_MANP -LARGEDURRY -NGC_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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                                                                    2, 2002, 20:29:55 ; Search time 61 Seconds (without alignments) 7431.207 Million cell updates/sec
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          GenCore version 5.1.3
Copyright (c) 1993 - 2002 Compugen Ltd
                                                  protein search, using frame_plus_n2p model
                                                                                                                                                                                                                                        hits satisfying chosen parameters:
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Ygapop 10.0 ,
Fgapop 6.0 ,
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Conservative:
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Indels:
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Best Local Similarity:
Query Match:
DB:
PROSITE; PS00038;
SEQUENCE 307 AA;
                                                  Alignment Scores:
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                          ch J.B., Wartman L., Bradfield C.A.;
of a Third Hypoxia Inducible Factor,
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alpha (Fragment).
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Mismatches:
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SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
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Matches:
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J. Biol. Chem. 0.0-0(1999).
EMBL, AR079143; AAF21782.1;
EMBL, AF079140; AAF21782.1;
EMBL, AF079141; AAF21782.1;
EMBL, AF079143; AAF21782.1;
UNED.
EMBL, AF079144; AAF21782.1;
UNED.
EMBL, AF079144; AAF21782.1;
UNED.
EMBL, AF079145; AAF21782.1;
UNINED.
EMBL, AF079146; AAF21782.1;
UNINED.
EMBL, AF079146; AAF21782.1;
UNINED.
EMBL, AF079149; AAF21782.1;
UNINED.
EMBL, AF079149; AAF21782.1;
UNINED.
EMBL, AF079150; AAF21782.1;
UNINED.
EMBL, AF0791516;
EMBL, AF0791516.1;
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EMBL, AF079151;
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EMBL, AF079151;
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EMBL, AF079151;
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                                                                                                                                                                                                                                                                          [1]
SEQUENCE FROM N.A.
Gu Y.-Z., Moran S.M., Hogenesch
"Cloning and Characterization of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR001610; PAC.
InterPro; IPR000014; PAS_domain.
Pfam; PF00989; PAS; 2.
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Length:
Matches:
Conservative:
Mismatches:
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                    7.93e-84
1045.00
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                           No.:
  Alignment :
Pred. No.:
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                    SMART; SW00086; PAC; 1.
SWART; SM00091; PAS; 2.
PROSTIE: PS00038; HELIX_LOOP_HELIX; UNKNOWN 1.
SEQUENCE 662 AA; 73013 MW; 58740A1B6993D3B5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q92215 PRELIMINARY; PRT; 662 AA. 092215; 01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAR-1999 (TrEMBLrel. 10, Last sequence update) 01-MAR-2002 (TrEMBLrel. 20, Last annotation update) Hypoxia inducible factor three alpha. HIF3A. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ------CAGCTCCCCTTCCACGATGGTGCTACTCTG 771
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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218
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31
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Inhibitory PAS domain protein.
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RESULT 5
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                 EMBL/GenBank/DDBJ databases
                                                                                                                                                      9665BOAF3998F8EF CRC64;
                                           'Cloning and characterization of human inhibitory PAS protein.";
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212
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                                                                        EMBL; AF463492; AAL69947.1; ...
InterPro; IPR001092; HLH_basic.
InterPro; IPR001014; PAS_domain.
Pfam; PF00989; PAS; 2.
SWART; SM00353; HLH; 1.
SWART; SM00091; PAS; 2.
PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
PROSITE; PS00102; PAS; 2.
SEQUENCE 632 AA; 68964 MW; 966580AF3998FBFF C
                                                                                                                                                                                 Length:
Matches:
Conservative:
Mismatches:
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Submitted (DEC-2001) to the
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1015.50
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Query Match:
         NCBI_TaxID=9606;
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TISSUE—OVARIAN CARCINOMA;

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

ISOGAI T., Nagai K., Sugano S., Ishibashi T., Fulimori K.,

A Nishikawa T., Nagai K., Suganobe M., Hiraoka S., Ishii S., Kawai Y.,

A Tanai H., Kimata M., Watamabe M., Hiraoka S., Ishii S., Kawai Y.,

A Saito K., Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K.,

A Masuho Y., Kanehori K.;

I MEDO human cDNA sequencing project.";

Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

EMBL: AK027755; BABS5244.1; -.

IN InterPro; IPR001010; PAC.

IN InterPro; IPR001010; PAC.

IN INTERPO; PR000010; PAC.

R InterPro; IPR000019; PAS.

PERM: PR000089; PAS.; 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        244 AGGGGGAGAGCCACTGGACGCCTGCTGAAGGCCCTGGAGGGTTTCGTCATGGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          aGlyGlyGluProLeuAspAlaCysTyrLeuLysAlaLeuGlyGlyPheValMetValLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GACGCGGCCCGCAGCCGCCAGCCAGCAGGAGGTGCTGTACCAGCTGGCGCACACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21 AspAlaAlaArgSerArgArgSerGlnGluThrGluValLeuTyrGlnLeuAlaHisThr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Euteleostomi;
Homo.
                                                                                                                                                                                                                                                                      S
                                                                                                                                                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DT-2002 (TrEMBLrel. 11, Last annotation update)
CDNA FLJ14819 fis, clone OWARC1000241, moderately similar hypoxia-inducible factor 1 alpha.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
632 AA; 68934 MW; A19F1ED3D05E7A71 CRC64;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                          22 IleCysGluAlaIlePro------HisProGlySer 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches:
Conservative:
Mismatches:
                                                          ATCTGTGAAGCCATCCCCCAGCTCCCCTTCCACGATGGTGCT
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                                                                                                                                                                          PRT;
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1011.50
84.77%
82.42%
50.32%
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Best Local Similarity:
Query Match:
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GCACAGACTTCCCCTGCCGGGAGCCCTCGCTCCGAGCCTCCCCTGCAATGCCTGGTGCTT 723
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                                                                                                                                    u--GluLeulleGlyHisSerllePheAspPheIleHisProCysAspGlnGluLeu
                                                             244 AGGGGGAGAGCCACTGGACGCCTGCTACCTGAAGGCCCTGGAGGGTTTCGTCATGGTACT
                           CAAGACGCCCTGACCCCCAGGCCGAACCTGTCAAAGAAGAAGCTGGAAGCCCCAACAGAG
                                                                                                                                                                                                 CGCCACTTTTCCCTGCGAATGAAGAGCACGCTCACCAGCAGAGGGCGCACGCTCAACCTC
                                                                                                                                                                                                                                   AAAGCGGCCACCTGGAAGGTGCTGCACTCAGGACATATGAGGGCCTACAAGCCCCCT
                                                                                                                                                                                                                                                                                                                                                            -------SerLeuGluProProLeu-GlyArgGlyAlaPhe---LeuSe
IleSerTyrLeuArgMetHisArgLeuCysAlaAlaGlyGluTrpAsnGlnValGly-Al
                                                                                       TCAGTGGACCTCTGTTCCTCCTCCTGATACATAACCCCACTCCTGGTACCAATTTCTCT
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Q9JHS2;
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                                          01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 40.0 kDa protein.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                     CAAGACGCCCTGACCCCCAGGCCGAACCTGTCAAAGAAGAAGCTGGAAGCCCCAACAGAG
                                                                                                        CGCCACTTTCCCTGCGAATGAAGAGCACGCTCACCAGCAGGGGGGCGCACGCTCAACCTC
                                                                                                                                           AAAGCGGCCACCTGGAAGGTGCTGCTCCTCAGGACATATGAGGGCCTACAAGCCCCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCAGTGGACCTCTGTTCCTCCTCCCTGATACATAACCCCACTCCTGGTACCAATTTCTCT
                                 Strausberg R.;
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL: BC0056308; AAH26308.1; -
Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                                                                                                            363 AA; 40020 MW; 15792F66151B612A CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                                                       363
236
11
39
80
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Matches:
Conservative:
Mismatches:
Indels:
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1007.00
67.49%
64.48%
50.10%
                120 rGln-----
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Best Local Similarity:
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Pred. No.:
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263 yTyrSerProAspAspLeuIleGlyCysSerAlaTyrGluTyrIleHisAlaLeuAspSe 283
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                                                                                                                                                                                                                                                                                                                   GGCTAGGAGGAGTGAAGGACATGGCCCAGCTATCCTTAGCCCAGAAACCCAAAATGTC
AAGAGGTGGCCTG--------TTCAGGTGCTACAGGGAAAGGG
                                                                       243 rArgHisSerLeuAspMetLysPheThrTyrCysAspAspArgIleAlaGluValAlaGl
                                                                                                                                                                                                                                                                                                                                                                                                   283 rAspAlaValSerLysSerIleHisThrCysMetTyrProIleSerPro-----
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UNW-2002 (TrEMBLrel. 21, Last annotation update)
Hypoxia inducible factor 3 alpha.
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CACTGCTCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCTGCCGGGAGC

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                                          MINIONE-21134367; PubMed-11237857;

A Kietzmann T., Cornesse Y., Brechtel K., Modaressi S., Jungermann K.;

Terivenous expression of the mRNA of the three hypoxia-inducible factor a-subunits HIF-1a, HIF2a and HIF3a in rat liver.";

E GAGLOREN, J. 354:531-537(2001).

E Biochem. J. 354:531-537(2001).

R InterPro; IPR001067; Nuc_translocat.

InterPro; IPR001067; Nuc_translocat.

R InterPro; IPR001067; Nuc_translocat.

R InterPro; IPR00104; PAS.

R PRINTS; PR007055; NCTRNSLOCATR.

R SMART; SM0036; PAC; 1.

R SMART; SM0036; PAC; 1.

R SMART; SM0036; PAC; 1.

R SMART; SM0038; HELLY. LOOP_HELLX; UNKNOWN_1.

R SMART; SM0038; HELLX.

R SMART; SM0038; HELLX.
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                47 AlaHisLeuAspLysAlaSerIleMetArgLeuThrIlleSerTyrLeuArgMetHisArg
                                                                                                                                                                                                                                                                                                                                                                                                                                    268 CTACCTGAAGGCCCTGGAGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATGGCTTA
                                                                                                                                                                                                                                                                                                                                                           223 CTCTGCGCAGCAGGTGGAA-------AAAGGGGGGAGAGCCCACTGGACGCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            448 TITGATITIAICCAICCCIGIGACCAAGAGGAACTICAAGACGCCCTGACCCCCAGGCCG
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211
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31
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Matches:
Conservative:
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Indels:
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83.928
82.758
49.808
                          FROM N.A.
                                                                                                                                                                                                                                          Percent Similarity:
Best Local Similarity:
                                     TISSUE-LIVER;
                                                                                                                                                                                                                  Alignment Scores:
                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     163
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Lamerdin J.E., McCready P.M., Skowronski E., Viswanathan V., Burkhart-Schultz K.J., Gordon L., Dias J., Ramirez M., Stilwagen S. Phan H., Velasco N., Do L., Regala W., Terry A., Garnes J., Danganan L., Erler A., Christensen M., Georgescu A., Avila J., Liu Attix C., Andreise T., Trankheim M., Amlco-Keller G., Coefield J., Duarte S., Lucas S., Bruce R., Thomas P., Quan G., Kronmiller B., Arellano A., Sanders C., Ow D., Nolan M., Trong S., Kobayashi A., Olsen A.S., Carrano A.V.;
CCTCGCTCCGAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hara S., Kobayashi C., Hamada J., Imura N.;
"Characterization of human hypoxia-inducible factor-3 alpha.";
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AC001193; AAD22668.1; -.
EMBL, AR054067; BAB69689.1; -.
InterPro; IPR001092; HLH_basic.
InterPro; IPR001067; Nuc_translocat.
InterPro; IPR001019; PAS_domain.
Pf00899; PAS; 2.
                                                                                                                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
inducible factor three alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
667 AA; 72404 MW; 67B8794FF9DCCF4B CRC64;
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205
6
7
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Mismatches:
Indels:
                                                                                                                                                       742 ------CAGCTCCCTTCCACGATGGTGCTACTCTG 771
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                                                                                                                                                                                                                                                                                                                                     Created)
                                                                                                                                                                                                                                                                                                                                                                                                                    (Hypoxia-inducible factor-3 alpha).
                                                                                                                                                                                                                                                                                           PRT;
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                                                                                                                                                                                                                                                                                                                              01-NOV-1999 (TrEMBLrel. 12, 01-NOV-1999 (TrEMBLrel. 12, 01-MAR-2002 (TrEMBLrel. 20, Putative homolog of hypoxia
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982.50
85.08%
82.66%
48.88%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
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Best Local Similarity:
Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMART: SM00091;
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SEQUENCE
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Alignment Scores:
Pred. No.:
  InterPro;
InterPro;
                                                                                                                   Match:
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                                                                                        Score:
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ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,
Nagai T., Ota T., Hayashi K., Sugano S., Shiratori A., Sudo H.,
Najatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,
Takahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi S.,
Matanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K.,
Yamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y.,
Ninomiya K., Iwayanagi T.;
Ninomiya K., Iwayanagi T.;
Ninomiya K., Iwayanagi T.;
Submitted (AUG 2000) to the EMBL/GenBank/DDBJ databases.
EMBL, AKO21653; BAB13865.1;
                                                                                                                  CTACCTGAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATGGCTTA 327
                  46
                                                         99
                                                                                                86
                                                TITGATITITATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGGCCG
                                                                                                                                                                                                                                                                                                                                                                   CCTCGCTCCGAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCCCAGCTC
                                                                                                                                                                                                                                                                                                                                                                                                          GCGCACCTGGACAAGGCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGC
                                                                             ------GGAAAAAGGGGGAGGCCACTGGACGCCTG
                                                                                       CTGATACATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGACACAGTATC
                                                                                                                                                                                                                                                                           AACCTGTCAAAGAAGAAGCTGGAAGCCCCAACAGAGCGCCACTTTTCCCTGCGAATGAAG
                                                                                                                                                                                                                                                                                                                   AGCACGCTCACCAGCAGGGGGGGCGCTCAACCTCAAAGCGGCCACCTGGAAGGTGCTG
CAGGAGACGGAGGTGCTGTACCAGCTGGCGCACACTCTGCCCCTTTGCGCGCGGCGTCAGC
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
Hypothetical 70.0 kDa protein.
Hypothetical 70.0 kDa protein.
Homo sapiens (Human.)
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Butele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                648 AA
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                                                                            CTCTGCGCAGCAGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
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Q9HAI2
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------Leu--GluLeuIleGlyHisSerIlePheAspPheIleHisProCysAsp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9HAM5;
01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
Hypothetical 21.6 kDa protein.
                                                                                                                                                                                                                                                                                                                                -----GGAAAAAGGGGGAGAGCCACTGGACGCCTGCTACCTGAAGGCCCTGGAGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                              CCTGGGCCTCAGTCAGTGGACCTCTGTTCCTCCTCCCTGATACATAACCCCACTCCTGGT
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TISSUE=EMBRYO;
Isogai T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki
                                                                              EBEFC744BC3F148E CRC64;
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158
6
6
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Matches:
Conservative:
Mismatches:
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                 _domain
                        LINEARTY SMO0089; PAS; 2.
SMART; SMO0081; PAS; 1.
SMART; SM00091; PAS; 2.
SROHENCE 648 AA; 69994 MW;
                                                                                                                        4.82e-58
753.50
82.00%
79.00%
37.49%
IPR001610; PAC.
IPR000014; PAS_
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Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    382
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203 GCTACCTGCGCATGCACCGCCTCTGCGCAGCAGGGGAAAAAGGGGGGAGAGCCACTGGAC 262
                                                                                                                                                                                                                                                                                                                        263 GCCTGCTACCTGAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATG 322
                                                                                                                                                                                                                                                                                                                                                                                                                            59
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                                                                                                                                                                                                                                                                                                                                                               383 CCTCCCTGATACATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGACACA
                                                                                                                                                                                                                                                                                                                                                                                                                 53 ------Leu--GluLeuIleGlyHiss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAGCCCTCGCAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        503 GCCCGAACCTGTCAAAGAAGAAGCTGGAAGCCCCAACAGAGCGCCCACTTTTCCCTGCGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 563 TGAAGAGCACGCTCACCAGCAGAGGGCGCACGTCAACCTCAAAGCGGCCACCTGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGCTGCACTGCTCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCTGCCG
                       Yamamoto J.,
Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Tamamoto J., Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.; "NEDO human CDNA sequencing project.";

"NEDO human CDNA sequencing project.";

EMBL; AK021421; BAB1391: - SEQUENCE 199 AA; 21597 MW; 646CB066A09B47C3 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequence update)
                                                                                                                Matches:
Conservative:
Mismatches:
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                                                                                                                                                Indels:
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                                                                                                    6.25e-51
672.00
64.19%
61.57%
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                                                                                                                        Percent Similarity:
Best Local Similarity:
                                                                                           Alignment Scores:
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Q9CYA8;
                                                                                                       Pred. No.:
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A Rawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S., Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Raio T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito T., Ashburner M., Batalov S., Casavant T., Raiota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Reischmann W., Gasterland T., Gissi C., King B., Kochiwa H., Ratsuo Y., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J., Rain I., M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., Sata IK., Okido T., Furuno M., Anno H., Baldarelli R., Barsh G., Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., Rothon P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.F., Sasaki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Mashizaki Y., Rawaji H., Kohtsuki S., Hasashaka Y., Kawaji H., Kohtsuki S., Hasashizaki Y., Rawaji W., Kawaji W., Kawaji
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                                                                                                                                      Eukaryota; Metaria; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBL_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 CAGCGCGTGAGGTCGAACACCGAGCTGCGGAAGGAGAAGTCGCGGGACGCGGCCCGCAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.
SEQUENCE 258 AA; 29703 MW; C42D1CD68117C552 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258
129
35
51
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01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypoxia inducible factor 1, alpha subunit.
HYPIA.
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Mismatches:
Indels:
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Matches:
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InterPro; IPR001092; HLH_basic.
InterPro; IPR001067; Nuc_translocat.
InterPro; IPR00014; PAS_domain.
Pfam; PF00989; PAS; 1.
SMART; SM00353; HLH; 1.
SMART; SM00091; PAS; 1.
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                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUE-EMBRYO;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nature 409:685-690(2001).
EMBL; AK017853; BAB30975.1; -.
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613.50
67.49%
53.09%
                                                                                                                         Mus musculus (Mouse)
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214 ATGCACCGCCTCTGCGCAGCAGGTGGAAAAAGGGGGAGAG
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01-NOV-1999 (TrEMBLrel. 12, Last seq.
01-MAR-2002 (TrEMBLrel. 20, Last anno
HYPOXIA-inducible factor-1 alpha.
HIF-1 ALPHA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=ARTERY;
MEDLINE=99255430; PubMed=10320777;
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01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypoxia inducible factor 1, alpha subunit.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                 CCCAGGCCGAACCTGTCAAAGAAGAAGCTGGAAGCCCCAACAGAGCGCCACTTTTCCCTG
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Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC026139; AAH26139.1; -.
SEQUENCE 836 AA; 93469 MW; 8A7B21B0F13E84D5 CRC64;
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129
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Matches:
Conservative:
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Indels:
Gaps:
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613.50
67.49%
53.09%
30.52%
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Best Local Similarity:
Query Match:
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|228 Pro 228
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319
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149
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--CCACT 258
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Hara S., Kobayashi C., Imura N.;
Hara S., Kobayashi C., Imura N.;
Halpha and -2alpha of bovine arterial endothelial cells.";
Halpha and -2alpha of bovine arterial endothelial cells.";
Biochim. Biophys. Acta 1445:237-243(1999).
Halpha and -2alpha of bovine arterial endothelial cells.";
EMBL; AB018398; BA78675.13 -.
InterPro; IPR001321; HypoxindFlA.
InterPro; IPR001321; HypoxindFlA.
InterPro; IPR001610; PAC.
Pfam; PF00785; PAC; 1.
Pfam; PF007899; PAS; 2.
                           88
                                                                                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Sukaryota: Metazooa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                      AAGGTGCTGCACTGCTCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCT
                  :: :::!!!
69 ValArgLysLeuLeuAspAlaGlyGly-LeuAspSerGluAspGluMetLysAlaGlnMe
                                                                                                                              379 TCCTCCTCCTGATACATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGA
                                                                                                                                                                                                                                                                                        499 CCCAGGCCGAACCTGTCAAAGAAGCTGGAAGCCCCCAACAGAGCGCCACTTTTCCCTG
                                                       GGACGCCTGCTACCTGAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGA
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(TrEMBLrel. 20, Last annotation update)
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SMART; SM00353; HLH; 1.
SMART; SM00086; PAC; 1.
SMART; SM00091; PAS; 2.
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NCBI_TaxID=9031;
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09YIB9;
01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 15, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypoxia-inducible factor-1 alpha.
Hypoxia-inducible factor-1 alpha.
Edalus gallus (Chicken).
Edalus qualus (Chicken).
Edalus Aetazoa (Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                        124
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                                                                                                                        GCAGCAGGTGGAAAAAGGGGGAGAG----------CCACTGGACGCCTGCTACCT
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                                                                                                                                                                                                                                                                                                                                                          454 ITTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGGCCGAACCTG
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                                                                                                                                                 213 LysLysProProMetThrCysLeuValLeuIleCysGluProllePro 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 694 TCCGAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCC 741
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195 ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnSerGlnCysGly-
PROSITE; PSO0038; HELIX_LOOP_HELIX; UNKNOWN_1. SEQUENCE 823 AA; 92127 MW; 12674E467A61B1A1 CRC64;
                                   823
130
33
47
28
                                  Length:
Matches:
Conservative:
                                                            Mismatches:
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                                                                                             US-09-896-791B-2 (1-1100) x Q9XTA5 (1-823)
                                 1.84e-45
611.50
68.49%
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                                                  The molecular cloning and expression of an avian cDNA for hypoxianiducible factor—1 alpha in embryonic ventricular myocytes.";
Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.
REMBL; ABO13746; BAA34234.2; -...
R InterPro; IPR001092; HLH_Dasic.
R InterPro; IPR00101610; PAC.
R InterPro; IPR00101610; PAC.
R InterPro; IPR001014; PAS_domain.
R Pfam; PF00785; PAC; 1.
R SMART; SM00086; PAC; 1.
R SMART; SM00086; PAC; 1.
R SMART; SM00086; PAS; 2.
R SMART; SM00081; PAS; 2.
R SMART; SM00091; PAS; 2.
C SMART; SM00091; PAS; 3.
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607.50
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SEQUENCE FROM
                     TISSUE-HEART;
                                      Takahashi T.:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LIVER;
Tanaka S., Sugimachi K.;
"Hypoxia-inducible factor-1 alpha variant isolated from human liver
                                                                                                                                      Eukaryota: Metazoa:
Mammalia: Butheria: Primates: Catarrhini: Hominidae: Homo.
NCBI_TaxID=9606;
         687 CCCTCGCTCCGAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCC 741
                                                                                                                                                                                                                        tissue.";
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; ABD73325; BAB70608.1; -
InterPro; IPR001092; HLL, basic.
InterPro; IPR001019; PAC.
InterPro; IPR001019; PAC.
InterPro; IPR001099; PAC.
InterPro; IPR001099; PAC.
R Pfam; PF00789; PAC; 1.
R Pfam; PF00989; PAC; 1.
SMART; SM00086; PAC; 1.
SMART; SM00086; PAC; 1.
SEQUENCE 735 AA; 82746 MW; 34DD604FB4E418E CRC64;
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129
33
48
28
                                                                       01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
HIPPAxia-inducible factor 1 alpha variant.
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Matches:
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Mismatches:
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606.50
68.078
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                                                          PRELIMINARY;
                                                                                                                                  Homo sapiens (Human)
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SEQUENCE FROM N.A.
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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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OM nucleic - protein search, using frame_plus_n2p model

2, 2002, 18:23:15 ; Search time 55.5 Seconds December

(without alignments) 5282.007 Million cell updates/sec

US-09-896-791B-2 2010 Perfect score:

......aaaaaaaaaaacatgcggccgc 1100 1 gaatteggcacgagggccat. sednence:

Scoring table:

0.5 0.5 7.0 0.7 BLOSUM62 Xgapop 10.0 , Xgapext Ygapop 10.0 , Ygapext Fgapop 6.0 , Fgapext Delop 6.0 , Delext

residues 908470 segs, 133250620 Searched:

Total number of hits satisfying chosen parameters:

length: 0 length: 2000000000 Minimum DB seq Maximum DB seq

Post-processing: Minimum Match 0%

Maximum Match 100% Listing first 45 summaries

Command line parameters:

-MODEL-frame+_n2p.model -DEV-xlp
-Q-C9012_1/102F0_28001/US0980591/runat_02122002_152657_5564/app_query.fasta_1.1287
-Q-C9012_1/102F0_28001/US09805991/runat_02122002_152657_5564/app_query.fasta_1.1287
-DB-A_Geneseq_101002 -OFMT-fastan -SUFFTX-rag -MINNATCH-0.1 -LOOPCL-0
-LOOPEXT-0 -UNITS-bits -START-1 -END--1 -MATRIX-blosum62 -TRANS-human40.cdi
-LIST-45 -DOCALIGN-200 -THR_SCORE-ptc -THR_MAX-100 -THR_MIN-0 -ALIGN-15
-UOSER-US09896791_6CGN_11_42_erunat_02122002_152657_5564 -NCPU-6 -ICPU-3
-NON-LOOPERT-0-1 -LARGEDGRRY -NGC_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT-120
-WARN_TIMEOUT-30 -THREADS-1 -XGAPOP-10 -XGAPEXT-0.5 -FGAPOP-6 -FGAPEXT-7

Jatabase :

1. (SIDSZ/gcgdata/geneseqp-embl/AA1980.DAT:*
2. (SIDSZ/gcgdata/geneseqp/geneseqp-embl/AA1981.DAT:*
3. (SIDSZ/gcgdata/geneseqp/geneseqp-embl/AA1981.DAT:*
4. (SIDSZ/gcgdata/geneseqy/geneseqp-embl/AA1981.DAT:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

HIF-Lathha variant
Human hypoxia indu
Amino acid sequenc
Human hypoxia-indu
A wild type human
Human lung tumour
Human Huri-lathha p A variant of human hypoxia-indu hypoxia-indu hypoxia-indu Clone #19080 of lu Lung small cell ca Murine endothelial Mouse inhibitory P A variant of human HIF-lalpha variant Human hypoxia-indu Mouse ischaemic co HIF-lalpha variant HIF-lalpha variant hypoxia-indu hypoxia-indu Human hypoxia-indu protein sequ HIF-3 protei Human protein segu Human protein segu novel Description Human Human Human Human Human Human Mouse Human AAY06289 AAY94640 AAU77613 AAU77615 AAU77616 AAY94636 AAW06557 AAU77612 AAY69407 AAE24212 AAU77608 AAU77617 Ω DB Length Query Match 101101 Result Ñ.

ALIGNMENTS

AAU75902 standard; Protein; 307 RESULT 1 AAU75902

AAU75902,

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Mouse inhibitory PAS domain (IPAS) protein. (first entry)

cardiovascular, cerebroprotective; ophthalmological; HiF-lalpha; hypoxia-induced factor lalpha; vascular endothelial growth factor; angiogenesis; ischaemic cardiovascular lesion; stroke; Inhibitory PAS domain protein; IPAS; cardiant; vasotropic;

Mus musculus

diabetic microvascular disease; tumour; mouse

WO200202609-A1

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CCCAGGCCGAACCTGTCAAAGAAGAAGCTGGAAGCCCCAACAAGAGCGCCCCTTTCCCTG 558
                                                                                                                                                                   CCCCAGCTCCCCTTCCACGATGGTGCTACTCTGGGTCTTCCACAGGAGAAGACTCCCATC
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                                                                                                                                                                                                                                      The invention describes an isolated nucleic acid encoding the biologically active inhibitory PAS domain protein or its functionally equivalent modifications. TPAS forms a non-functional heterodimeric complex with HIF-lalpha (hypoxia-induced factor lalpha), imparing interaction between HIF-lalpha and hypoxia-response elements in genes, e.g. the gene for vascular endothelial growth factor, so contributes to control of hypoxic signalling. The nucleic acid and its encoded polypeptides, are used to identify agents that activate expression of the gene or stimulate activity of the protein. These agents are useful for inhibiting angiogenesis, particularly where associated with ischaemic cardiovascular lesions, stroke or diabetic microvascular diseases, and tumour growth. This is the amino acid sequence of the mouse inhibitory PAS domain protein (IPAS), described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    258
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                                                                                                                                                           New nucleic acid encoding inhibitory PAS domain protein, useful for identifying specific inhibitors for treating e.g. anglogenesis or tumour growth \,
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                                                                                                                                                                                                                 Claim 3; Fig 1; 44pp; English.
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                       19-JUN-2001; 2001WO-SE01387
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N-PSDB; ABK14502.
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present sequence represents mouse MOP7, a novel member of the superfamily, where PAS stands for PER/ARNT/SIM domains. MOP7 $\,$ MOP7; member of the PAS superfamily; bHLH-PAS; mouse; transcription regulator; hypoxia inducible factor 3 alpha. proteins associated

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to identify bHLH-PAS proteins, and by RACE amplification of lung to identify bHLH-PAS proteins, and by RACE amplification of lung cDNA. MOP7 was characterised as hypoxia inducible factor 3 alpha (CDNA. MOP7 was characterised as hypoxia inducible factor 3 alpha (CHIF 3 alpha). Its expression profile is distinct from that of HIF 1 alpha (see AAY06289), HIF 2 alpha (see AAY06290), MOP3 (see AAY06291), Ah receptor and Ah receptor nuclear translocator (ARNT), suggesting a different functional role. MOP7 probably regulates the same genes as HIF 1 alpha and 2 alpha, as evidenced by its climerisation with the same partners (ARNT, MOP3) and recognition of the same core response element. MOP7 may have a functional cole the same core response element. MOP7 may have a functional cole associated with response to low oxygen in the tissues in which it is expressed. The invention provides novel MOPS 2-9 nucleic acids (see AAX58981-88) and proteins (see AAY06289-97). These are useful in a variety of response to diagnostic and the mops are alpha-class hypoxia-inducible factors. Others are involved in circadian signal
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polynucleotide which comprises a 3'-end sequence, where the combination of the 5'-end sequence, where the composes at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length CONAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length CONAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length AAH13613 to AAH13613 and AAH13613 to AAH13619 to AAH13619 to AAH3619 represent human amino acid sequences; and AAH3629 to AAH3619 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligoral primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprising a sequence complementary to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
741
                      Human; primer; detection; diagnosis; antisense therapy; gene therapy.
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  CCTCGCTCCGAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCC
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, Otsuki 7
                                                                                               228 AlaSerLeuGluProProLeuGlyArgGlyAlaPheLeu 240
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Sugiyama T, Wakamatsu A, Nagai K,
                                                                           -----CAGCTCCCCTTCCACGATGGTGCTACTCTG
                                                                                                                                                                                                                                                                                                                  sequence SEQ ID NO:12422.
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                                                                                                                                                                                               AAB93326 standard; Protein; 632
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27-AdG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-AMX-2000; 2000JP-0183767.
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                                                                                                              GACGCGCCCCCCCGCCGCCCAGGACGGAGGTGCTGTACCAGCTGGCGCACACT
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The invention relates to a method of treating a subject having or at risk of developing a haematologic malignancy or multidrug resistance (MDR). The method involves administering hypoxia inducible factor-1 (MIF-1) binding molecules or small ubiquitin-like-modifier (SUWO)-1 binding molecules or HIF-1-SUWO-1 complex modulators. mdr1-hypoxia responsive element (HRE) binding molecules or antisense uncleic acid molecules and SUMO-1 binding molecules or antisense molecules are useful for treating a subject having or at risk of developing haematologic malignancy or MDR (e.g. a lymphoid disorder or a myeloid chronic lymphopid disorders include lymphocytic leukaemia or chronic lymphoid leukaemia. The myeloid disorders e.g. lymphoma, myeloma or chronic lymphoid leukaemia. The myeloid disorders include chronic or acute myeloid leukaemia or e.g. anglogenic myeloid metaplasia, essential thrombocythaemia or polycythaemia vera. The invention is used in gene therapy. The present sequence is human HIF-3 protein.
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Human; haematologic malignancy; multidrug resistance; MDR; SUMO-1; hypoxia inducible factor-1; small ubiguitin-like-modifier; HIF-3; hymphoid disorder; chronic lymphoproliferative disorder; lymphoma; myeloid disorder; lymphocytic leukaemia; thrombocythaemia; myeloma; anglogenic myeloid metaplasia; myeloid leukaemia; gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                           or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     163 GCGCACCTGGACAAGGCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGC
                                                                                                                                                                                                                                                                                                                                                                                      Treating a subject (at risk of) having a hematologic malignancy omultidrug resistance, e.g. lymphoma or myeloma, by administering hypoxia inducible factor 1 binding molecules or small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          667
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                                                                                   polycythaemia vera; hypoxia responsive element; HRE
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                                                                                                                                                                                                                                                                             (BGHM ) BRIGHAM & WOMENS HOSPITAL INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 88-91; 92pp; English.
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                                                                                                                  Homo sapiens
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Human; inflammatory condition; shock; sepsis; immune response; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral softensis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder;
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Yamazaki V,
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The invention trainers to insign mover polymerical and associated treating inflammatory conditions such as arthritis, nephritis, Crohn's treating inflammatory conditions such as arthritis, nephritis, Crohn's disease, ischemnia repertusion injury, shock, sepsis, immune responses and cancer and for promoting wound healing. The sequences are used to brain tissue, and are useful for the treatment of central and paripheral consistence in diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral nervous system diseases and neuropathies, such as Alzheimer's disease, Parkinson's disease, Huntington's disease and amyotrophic lateral cortivity, regulation of haematopoiesis, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, cell disorders and platelet disorders such as thrombocytopenia, cell disorders and platelet disorders such as thrombocytopenia, cortivity, tissue repair, healing of burns, inclsions, ulcers, treatment of corteoporosis, osteoarthritis, bone degenerative disorders and periodontal disease. The sequences of the invention are also useful for gut corteoporosis, osteoarthritis, bone degenerative disorders and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autofimmune disorders engalishes clerosis and myasthenia gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABG66666-ABG666788 represent human coagulation disorders. Sequences asthma, thrombolysis or thrombosis conversed to a sequence of the invention.
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                                                                                                                                                                         invention relates to human novel polynucleotides and associated
                                                      of
cell
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                                                  Novel nucleic acids and polypeptides for diagnosis, treatment inflammatory, autoimmune, nervous system, myeloid or lymphoid disorders, cancer and promoting wound healing -
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Best Local Similarity:
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                                                                                           CTGTCAAAGAAGAGGCTGGAAGCCCCAACAGAGCGCCCACTTTTCCCTGCGAATGAAGAGC
                                                   ACGCTCACCAGCAGGGGGCGCACGCTCAACCTCAAAGCGGCCACCTGGAAGGTGCTGCAC
                                                                                                                          TGCTCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCTGCCGGGAGCCCT
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                                                                                                                                                                                                                                                                                                 ------TTCAGGTGCTACAGGGGAAAGGGACTGAATCCT-------
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2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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The present invention describes primer sets for synthesising 5602
[ull-length cDNas defined in the specification. Where a primer set
comprises: (a) an oligo-dT primer and an oligonucleotide complementary
to the complementary strand of a polynucleotide which comprises one of
the 5602 nucleotide sequences defined in the specification, where the
coligonucleotide comprises at least 15 nucleotides; or (b) a combination
of an oligonucleotide comprises a sequence complementary to the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprising a sequence complementary to a
polynucleotide which comprises a 1'-end sequence. Where the
complementary strand of a polynucleotide which comprises a 5'-end
sequence and an oligonucleotide comprises and the combination of
the specification. The primer sets selected from those defined in
the specification. The primer sets can be used in antisense therapy and
in gene therapy. The primer sets can be used in antisense therapy and
in gene therapy. The primers are useful for synthesising polynucleotides,
particularly full-length cDNAs. The primers are also useful for the
cubnAs easily without any specialised methods. AAH03632 and
AAH03633 to AAH18742 represent human cDNA sequences; AAB9446 to
AAH03633 represent human amino acid sequences; and AAH13632
crepresent oligonucleotides, all of which are used in the exemplification
                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21 GlnValGly-AlaGlyGlyGlyGlvDroLeuAspAlaCysTyrLeuLysAlaLeuGluGlyPh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 MetargLeuThrIleSerTyrLeuArgMetHisArgLeuCysAlaAlaGlyGluTrpAsn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----GGAAAAAGGGGGAGACCACTGGACGCCTGCTACCTGAAGGCCCTGGAGGGTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAAGAGGAACTTCAAGACGCCCTGACCCCAGGCCGAACCTGTCAAAGAAGAAGCTGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCCCAACAGAGGGCCACTTTTCCCTGCGAATGAAGAGCACGCTCACCAGCAGAGGGGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             187 ATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGCGCAGCAGGT-
 <u>:</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches:
Conservative:
Mismatches:
                                                                                                                                                                  Claim 8; SEQ ID 16415; 2537pp + CD ROM; English.
 Nagai K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-896-791B-2 (1-1100) x AAB94934 (1-648)
Wakamatsu A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.56e-59
753.50
82.00%
79.00%
37.49%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the present invention.
Sugiyama T,
                                    WPI; 2001-318749/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Alignment Scores:
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shii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match:
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QQ

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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comparises: (a) an oilgo-dT primer and an oilgouncleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide comprises at least 15 nucleotides; or (b) a combination of an oilgonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 3'-end sequence and an oilgonucleotide comprising a sequence complementary to a polynucleotide which comprises a 3'-end sequence. Where the oilgonucleotide which comprises a 3'-end sequence complementary to a polynucleotide which comprises a 3'-end sequence. Where the oilgonucleotide which comprises a 1'-end sequence is selected from those defined in the 5'-end sequence/3'-end sequence is selected from those defined in the primer sets can be used in antisense therapy and in gene therapy. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs. The primers allow obtaining of the full-length cDNAs as asily without any specialised methods. AAH13629 to AAH13632 AAH13631 represent human amino acid sequences; and AAH13629 to AAH13632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
 651
                     711
                                                                                          detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamamoto J;
 ACGCTCAACCTCAAAGCGGCCACCTGGAAGGTGCTGCACTGCTCAGGACATATGAGGGCC
                                                                       TACAAGCCCCCTGCACAGACTTCCCCTGCCGGGAGCCCTCGCTCCGAGCCTCCCTGCAA
                                                                                                                                            Saito K, Ya
Otsuki T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 8; SEQ ID 13303; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashi K, Sa
A, Nagai K,
                                                                                                                                                                                                                                                                                                                                                                     Human protein sequence SEQ ID NO:13303
                                                                                                                                                                                                                                                       AAB93710 standard; Protein; 199 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T, Nishikawa T,
Sugiyama T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2000JP-0118776.
2000JP-0183767.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                         Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-JUL-1999;
27-AUG-1999;
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02-MAY-2000;
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Ishii S,
                                                                                                                                                                                                                                                                                            AAB93710;
592
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the exemplification
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                                                                                                                                                                                                                       202
                                                                                                                                                                                                                                                                   262
                                                                                                                                                                                                                                                                                                              263 GCCTGCTACCTGAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATG 322
                                                                                                                                                                                                                                                                                                                                                             382
                                                                                                                                                                                                                                                                                                                                                                                                        442
                                                                                                                                                                                                                                                                                                                                                                                                                                                    443 GTATCTTTGATTTTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCA 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                503 GGCCGAACCTGTCAAAGAAGAAGCTGGAAGCCCCAACAGAGCGCCCACTTTTCCCTGCGAA 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
                                                                                                                                                                                                                                                                                                                                                                                                                     2 ArgProAlaAlaGlyAlaAlaArgArgProArgCysCysThrSerTrpLeuThrArgCys
                                                                                                                                                                                                                       143 CCTTTGCGCGGGGGGTCAGCGCGCACCTGGACAAGGCCTCCATCATGCGCCTCACAATCA
                                                                                                                                                                                                                                            22 ProSerProAlaAlaSerAlaProThrTrpThrArgProLeuSerCysAlaSerProSer
                                                                                                                                                                                                                                                                   203 GCTACCTGCGCATGCACCGCCTCTGCGCAGGTGGAAAAAGGGGGAGAGCCACTGGAC
                                                                                                                                                                                                                                                                                                                                                           383 CCTCCCTGATACATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGACACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGAAGAGCACGCTCACCAGCAGAGGGCGCACGCTCAACCTCAAAGCGGCCACCTGGAAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          623 TGCTGCACTGCTCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCTGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     683 GGAGCCCTCGCTCCGAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mouse ischaemic condition related protein sequence SEQ ID NO:760.
                                                                       199
141
6
14
68
represent oligonucleotides, all of which are used in of the present invention.
                                                                                                                                                                                                                                                                                         42 AlaThrCysAlaCysThrAlaSerAlaProGln---------
                                                                                              Conservative:
                                                                                                        Mismatches:
                                                                        Length:
Matches:
                                                                                                                     Indels:
                                                                                                                                                     US-09-896-791B-2 (1-1100) x AAB93710 (1-199)
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                                                                                                                                                                                                                                                                               ABB57270 standard; Protein; 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGCTCCCCTTCCACGATGGTGCT
                                                                                672.00
64.19%
61.57%
33.43%
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                                                                                              Percent Similarity:
Best Local Similarity:
                                       199
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                                                             Alignment Scores:
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                                        Sequence
                                                                                                                   Query Match:
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     SSXS
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The present invention describes a method for examining ischaemic conditions, comprising measuring the expression levels of particular genes (I) in a test sample or determining the expression profile of a gene group in the sample comprising genes selected from (I). The method is useful for examining the ischaemic condition (e.g. compression is useful for examining the ischaemic condition (e.g. compression is useful for examining the ischaemic condition (e.g. compression texts of particular genes (AB199202 to AB199912, encoding the protein sequences in ABB57020 to ABB57374) or by determining the expression profile of a gene group comprising these genes. The capression profiles produced by these genes are used as an indicator when screening for ischaemic condition improving chuses or therapeutics for ischaemic diseases. AB199913 and AB199914 represent PCR primers for a mouse ischaemic condition related sequence, which are used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Examining the ischemic condition (e.g. occlusive ischemia) by measuring expression levels of particular genes defined in the specification or by determining the expression profile of a gene group comprising these
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGGAGGTGCTGTACCAGCTGGCGCACACTCTGCCCTTTGCGCGCGGCGTCAGCGCGCAC 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62 AspAlaGlyGly-LeuAspSerGluAspGluMetLysAlaGlnMetAspCysPheTyrLe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATGGCTTACCTGTC
Mouse; ischaemia; compressive ischaemia; occlusive ischaemia; vasospastic ischaemia; ischaemic condition; ischaemic disease.
                                                                                                                                                                                                                                                                                                                                                                                  Ishii Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           810
129
32
49
28
3
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Mismatches:
Indels:
                                                                                                                                                                                                                                                                                                                                                                           Takahashi Y, Nagata T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length:
Matches:
                                                                                                                                                                                                                                                                                                                            (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 2; Page 1869-1873; 2690pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-896-791B-2 (1-1100) x ABB57270 (1-810)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2.87e-46
610.50
67.65%
54.20%
30.37%
                                                                                                                                                                                                                              2001WO-JP04192.
                                                                                                                                                                                                                                                                          18-MAY-2000; 2000JP-0145977.
                                                                                                                                                                                                                                                                                                                                                                             Asai S,
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-034733/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; ABI99710
                                                                                                                     WO200188188-A2
                                                                      Mus musculus.
                                                                                                                                                                                                                        18-MAY-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                             Ishikawa K,
                                                                                                                                                                       22-NOV-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
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9
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This sequence represents a fragment of the hypoxia-inducible factor (HIF)-lalpha amino acid sequence. The mechanism of action of HIF-lalpha is a multi-step process which includes hypoxia-dependent nuclear import and activation of the transactivation domain. The HIF-lalpha consists of a number of functional domains including a PAS-B (Per, Arnt, Sim) domain located in human HIF-lalpha between amino acids 173 and 390, a C-terminal nuclear localization sequence located at amino acids 718-584, a transactivator domain (N-TAAD) located between amino acids 531 and 584, and a second transactivator domain (C-TAAD) located between 813 and 826.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human hypoxia-inducible factor alpha variants for identifying compounds that modulate its functional domain and regulate genes involved in
 GGAAAATGTCAGCAAGCACCTGGGCCTCAGTCAGTGGACCTCTGTTCCTCCTCCTGATA 393
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ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr 200
                                                                                                                                                                                                                                                                                                       TCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCTGCCGGGAGCCCTCGC 693
                                                                                                                       TTTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGGCCGAACCTG
                                                                                                                                    CATAACCCCACTCCTGGTACCAATTTCTCTGGAGCTCATTGGACACAGTATCTTTGAT
                                                                                                                                                                                                                                            CTCACCAGCAGAGGGCGCACGCTCAACCTCAAAGCGGCCACCTGGAAGGTGCTGCACTGC
                                                                                                                                                                                 TCAAAGAAGAAGCTGGAAGCCCCAACAGAGCGCCACTTTTCCCTGCGAATGAAGAGCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypoxia-inducible factor lalpha; HIF-lalpha; PAS-B; N-TAD; Cregulation; angiogenesis; erythropoiesis; glycolysis; human.
                                                                                                                                                                                                                                                                                                                                                                               TCCGAGCCTCCCCTGCAATGCCTGGTGTGTGAAGCCATCCCC 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HIF-lalpha variant protein sequence HIF-lalpha/1-245.
                  Claim 13; Page 68-69; 87pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY94627 standard; protein; 245
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AAY94628 standard; protein; 330

AAY94628;

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represented by the present sequence. The variants are useful for identifying compounds capable of modulating the function of a functional domain of human HFr-lalpha. The method comprises contacting a candidate compound with a cell expressing a HFr-lalpha variant conjugated to a molecular probe. The localization of the probe can be detected in the cell. The Aequeora victoria green fluorescent protein can be used as the molecular probe. The compounds are useful for the regulation of HFr-lalpha target genes, such as those involved in the regulation of anglogenesis, erythropoiesis an glycolysis.
  such as that
                                                                                                                                                                                                                                                                                               CTGGACAAGGCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGC 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          274 GAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGACATGGCTTACCTGTC 333
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195 ThrGlyHisTleHisValTyrAspThrAsnGerAsnGlnProGlnCysGly-----Tyr 212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        invention relates to isolated variants of HIF-lalpha,
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Mismatches:
Indels:
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Matches:
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RESULT 10 AAY94628

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This sequence represents a fragment of the hypoxia-inducible factor (HIF)-lalpha amino acid sequence. The mechanism of action of HIF-lalpha is a multi-step process which includes hypoxia-dependent nuclear import and activation of the transactivation domain. The HIF-lalpha consists of a number of functional domains including a PAS-B (Per, Arnt, Sim) domain located in human HIF-lalpha between amino acids 173 and 390, a C-terminal nuclear localization sequence located at amino acids 718-584, a transactivator domain (N-TAD) located between amino acids 531 and 584, and a second transactivator domain (C-TAD) located between 813 and 826. The invention relates to isolated variants of HIF-lalpha, such as that represented by the present sequence. The variants are useful for identifying compounds capable of modulating the function of a functional domain of human HIF-lalpha. The method comprises contacting a candidate compound with a cell expressing a HIF-lalpha variant conjugated to a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              molecular probe. The localization of the probe can be detected in the cell. The Aequeora victoria green fluorescent protein can be used as the molecular probe. The compounds are useful for the regulation of HIF-lalpha target genes, such as those involved in the regulation of
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human hypoxia-inducible factor alpha variants for identifying compounds that modulate its functional domain and regulate genes involved in angiogenesis, erythropoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        49 AACACCGAGCTGCGGAAGGAGAGTCGCGGGACGCGGCCCGCAGCCGGCGCGCAGCCAGGAG 108
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                                                                                                                                                   regulation; angiogenesis; erythropolesis; glycolysis; human.
                                                                                                                                 Hypoxia-inducible factor lalpha; HIF-lalpha; PAS-B; N-TAD;
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             Aspalagly-AspLeuAspIleGluAspAspMetLysAlaGlnMetAsnCysPheTyrLe
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ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia; ischemia related damage; angiogenesis; coronary artery disease; ischemic tissue damage.
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GGAAAATGTCAGCAACCTGGGCCTCAGTCAGTGGACCTCTGTTCCTCCTCCTCGTGATA 393

63 334 394 CATAACCCCACTCCTGGTACCAATTTCTCTGGAGCTCATTGGACACACTATGAT

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514 TCAAAGAAGAAGCTGGAAGCCCCAACAGAGCGCCACTTTTCCCTGCGAATGAAGAGCACG

454 TITATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGGCCGAACCTG

574 CICACCAGCAGAGGCGCACGCICAACCICAAAGCGGCCACCTGGAAGGIGCTGCACTGC

333

93

74 AspAlaGly-AspLeuAspIleGluAspAspMetLysAlaGlnMetAsnCysPheTyrLe 274 GAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGAACATGGCTTACCTGTC

g οy qq Qγ g Qγ g δ 요 ò Db QΥ qq

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The present sequence represents a variant of hypoxia-inducible factor (HIF)-1 alpha, comprising amino acids 1-391 and 576-826 of the wild type protein (see AAY69407). The HIF-lalpha variants are stable under hypoxic and non-hypoxic conditions. The variants comprises amino acid residues 1:391 and 521-826, 549-826, 429-826, 469-826, 494-826, 508-826, 512-826 or 517-826 of the wild type human HIF-lalpha collypeptide, in which residues 551 and 52 are not serine and threonine, respectively. The HIF-lalpha variant polynucleotide sequences are useful for increasing expression of a hypoxia inducible gene in a cell. They is also useful for providing constitutive expression of a hypoxia inducible factor in a cell, and for reducing or preventing hypoxia or inducible factor in a cell, and for reducing or preventing hypoxia or is size the constitutive expression of a hypoxia or is commis related damage. The variant HIF-lalpha polypeptides are useful for providing prophylactic therapy for inducible the level of angences in tissues of patients at risk of coronary artery disease
                                                                                                                                                                                                                                                                                                                                                 note: this sequence does not appear in the specification; it was created
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        168
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treating hypoxia or ischemia-related tissue damage
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                                    Claim 1; Page -; 96pp; English.
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606.50
68.07$
54.208
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DB:
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Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This sequence represents a fragment of the hypoxia-inducible factor (HIF)-lalpha amino acid sequence. The mechanism of action of HIF-lalpha consists of sa multi-step process which includes hypoxia-dependent nuclear import and activation of the transactivation domain. The HIF-lalpha consists of number of functional domains including a PAS-B (Per. Arnt, Sin) domain conclear localization sequence located at amino acids 718-584, a nuclear localization sequence located between amino acids 718-584, a transactivator domain (N-TAD) located between amino acids 33 and 580, and a second transactivator domain (C-TAD) located between 813 and 826. The invention relates to isolated variants of HIF-lalpha, variants of the invention relates to isolated variants of HIF-lalpha, when the present sequence. The variants are useful for represented by the present sequence. The variants are useful for domain of human HIF-lalpha ariant compacting a candidate compound with a cell expressing a HIF-lalpha variant conjugated to a compound with a cell expressing a HIF-lalpha variant conjugated to a conjuctular probe. The localization of the probe can be detected in the coll. The Aequencar victoria green fluorescent protein can be used as the compound a probe. The compounds are useful for the regulation of HIF-lalpha target genes, such as those involved in the regulation of anglogenesis, erythropoiesis an glycolysis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human hypoxia-inducible factor alpha variants for identifying compounds that modulate its functional domain and regulate genes involved in
               :::|||||||:::
195 ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr 212
634 TCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCTGCCGGGAGCCCTCGC 693
                                                                                                                                                                                                                                              Hypoxia-inducible factor lalpha; HIF-lalpha; PAS-B; N-TAD; C-TAD; regulation; anglogenesis; erythropoiesis; glycolysis; human.
                                                                 694 TCCGAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCC 741
                                                                                                                                                                                                                   HIF-lalpha variant protein sequence HIF-lalpha/1-652.
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Matches:
Conservative:
Mismatches:
Indels:
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                                                                                                                                    AAY94629 standard; protein; 652 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anglogenesis, erythropoiesis -
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30.17%
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                                                                                                                                                                                         (first entry)
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Best Local Similarity:
Query Match:
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                                                                                                                                                                                                                                                                                       Homo sapiens.
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513
                                            169 CTGGACAAGGCCTCCATCATGCGCCTCACAATCAGCTACCTGCGCATGCACCGCCTCTGC 228
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                                                                                                                                                                                                                                                                                                                                                                                        274 GAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGGAGCATGGCTTACCTGTC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             334 GGAAAATGTCAGCAAGCACCTGGGCCTCAGTCAGTGGACCTCTGTTCCTCCTCCTGATA 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               394 CATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGACACAGTATCTTTGAT 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 SerGluValPheTyrGluLeuAlaHisGlnLeuProLeuProHisAsnValSerSerHis
                                                                                                                                                                                                                                                                                                                              -- CCACTGGACGCCTGCTACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              454 TTTATCCATCCCTGTGACCAAGGAACTTCAAGACGCCCTGACCCCCAGGCCGAACCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        514 TCAAAGAAGAAGCTGGAAGCCCCAACAGAGCGCCACTTTTCCCTGCGAATGAAGAGACACG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             634 TCAGGACATATGAGGGCCTACAAGCCCCTGCACAGACTTCCCCTGCCGGGAGCCCTCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia; ischemia related damage; angiogenesis; coronary artery disease; ischemic tissue damage.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A variant of human hypoxia inducible factor-1. alpha protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      694 TCCGAGCCTCCCCTGCAATGCCTGGTGCTTATCTGTGAAGCCATCCCC 741
US-09-896-791B-2 (1-1100) x AAY94629 (1-652)
                                                                                                                                                                                                                                                                                                      229 GCAGCAGGTGGAAAAAGGGGGAGAG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY84167 standard; Protein; 669 AA.
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                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a variant of hypoxia-inducible factor (HIF) 1 alpha, comprising amino acids 1-391 and 549-826 of the wild type protein (see AAX69407). The HIF-lalpha variants are stable under hypoxic and non-hypoxic conditions. The variants comprises amino acid residues 1-391 and 521-826, 549-826, 478-826, 429-826, 469-826, 698-826, 512-826 or 517-826 of the wild type human HIF-lalpha acid polypeptide, in which residues 531 and 522 are not serine and threonine, respectively. The HIF-lalpha variant polynucleotide sequences are useful for increasing expression of a hypoxia inducible gene in a cell. They is also useful for providing constitutive expression of a hypoxia inducible factor in a cell, and for reducing or preventing hypoxia or ischemia related damage. The variant HIF-lalpha polypeptides are useful for providing prophylactic therapy for inducible the level of any prophylactic therapy for inducing the level of any prophylactic therapy and 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               not appear in the specification; it was created
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   --CCACTGGACGCCTGCTACCT
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1129
33
48
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                                                                                                                                                                                                                                                                      treating hypoxia or ischemia-related tissue damage
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Matches:
Conservative:
Mismatches:
                                                                                               JOHNS HOPKINS SCHOOL MEDICINE
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                                                                                                                                                                                                                                                                                                              Claim 1; Page -; 96pp; English.
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  99WO-US19416.
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54.20%
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        or ischemic tissue damage.
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Best Local Similarity:
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                                                                                               VINU ( OLYU)
  25-AUG-1999;
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                                                                                                                                              Semenza GL;
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The present sequence represents a variant of hypoxia-inducible factor (HIF)-1 alpha, comprising amino acids 1-391 and 521-826 of the wild type protein (see AAY69407). The HIF-lalpha variants are stable under hypoxic and non-hypoxic conditions. The variants comprises amino acid residues 1-391 and 521-826, 549-826, 576-826, 429-826, 469-826, 494-826, 508-826, 512-826 or 517-826 of the wild type human HIF-lalpha polypeptide, in which residues 551 and 552 are not serine and threonine, respectively. The HIF-lalpha variant polynucleotide sequences are useful
TTTATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGGCCGAACCTG 513
                 TCAGGACATATGAGGGCCTACAAGCCCCCTGCACAGACTTCCCCTGCCGGGAGCCCTCGC 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
treating hypoxia or ischemia-related tissue damage -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is.
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ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
                                                           TCAAAGAAGAAGCTGGAAGCCCCCAACAGAGCGCCACTTTTCCCTGCGAATGAAGAGCACG
                                                                                                                    CTCACCAGCAGAGGGGGCACGCTCAACCTCAAAGCGGCCACCTGGAAGGTGCTGCACTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia; ischemia related damage; angiogenesis; coronary artery disease; ischemic tissue damage.
                                                                                                                                                                                                                                                                                                                                                                                                                     A variant of human hypoxia inducible factor-1 alpha protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "this residue is optionally not Ser, preferably Gly"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             423 . This residue is optionally not Thr, preferably Ala"
                                                                                                                                                                                                                                    UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
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454
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AAY84173;

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                                                                                                         or ischemic tissue damage.
note: this sequence does not appear in the specification; it was created
using information provided.
                                                     polypeptides are useful
the level of
for increasing expression of a hypoxia inducible gene in a cell. They is also useful for providing constitutive expression of a hypoxia inducible factor in a cell, and for reducing or preventing hypoxia or ischemia related damage. The variant HFF-lalpha polypeptides are useful for providing prophylactic therapy for inducing the level of analysions of patients at risk of coronary artery disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GAAGGCCCTGGAGGGTTTCGTCATGGTACTCACCGCCGAGGAGACATGGCTTACCTGTC 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  513
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54.20%
                                                                                                                                                                                     697 AA;
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Best Local Similarity:
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The present sequence represents a variant of hypoxia-inducible factor (HIF) 1 alpha, comprising amino acids 1.391 and 517-826 of the wild type protein (see AAY69407). The HIF-lalpha variants are stable under hypoxic and non-hypoxic conditions. The variants comprises amino acid residues 1.391 and 521-826, 549-826, 429-826, 469-826, 494-826, 508-826, 512-826 or 517-826 of the wild type human HIF-lalpha threonine, polypeptide, in which residues 531 and 552 are not serine and threonine, respectively. The HIF-lalpha variant polynucleotide sequences are useful for increasing expression of a hypoxia inducible gene in a cell. They is also useful for providing constitutive expression of a hypoxia (inducible factor in a cell, and for reducing or preventing hypoxia or ischemia related damage. The variant HIF-lalpha polypeptides are useful for providing prophylactic therapy for inducible the level of any or increasing in tissues of patients at risk of coronary artery disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence does not appear in the specification; it was created
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Variant forms of hypoxia-inducible factor (HIF)-1 alpha, useful for
                                                                                          Human; hypoxia-inducible factor 1 alpha; HIF-lalpha; variant; hypoxia inducible gene; hypoxia inducible factor; hypoxia; ischemia related damage; angiogenesis; coronary artery disease;
                                               A variant of human hypoxia inducible factor-1 alpha protein
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preferably Gly"
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preferably Ala"
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                                                                                                                                                                                                                                                                                Location/Qualifiers
Misc-difference 426
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(first entry)
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                                                                                                                                                                      CATAACCCCACTCCTGGTACCAATTTCTCTCTGGAGCTCATTGGACACAGTATCTTTGAT 453
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ThrGlyHisIleHisValTyrAspThrAsnSerAsnGlnProGlnCysGly-----Tyr
                        TITATCCATCCCTGTGACCAAGAGGAACTTCAAGACGCCCTGACCCCCAGGCCGAACCTG
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